

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2005, 07:16:57 ; Search time 118.905 Seconds

(without alignments)
325.267 Million cell updates/sec

Title: US-09-743-818A-4_COPY_1_100

Perfect score: 524
Sequence: 1 SMGVPALPGVPGVFPV.....AAKAGAGLGVPGVGLGVIS 100Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	524	100.0	733	2	AAR56653 Synthetic
2	524	100.0	733	2	AAY01301 Amino aci
3	515	98.3	515	3	AAY69135 Amino aci
4	515	98.3	571	3	AAY69071 Amino aci
5	515	98.3	692	7	ADE40134 Human NOV
6	515	98.3	698	2	AAY01302 Human tro
7	515	98.3	698	3	AAY69069 Amino aci
8	515	98.3	711	7	ADE40132 Human NOV
9	515	98.3	712	3	AAB08630 Amino aci
10	515	98.3	730	2	AAW46315 Human ela
11	515	98.3	730	3	AAB08631 Fusion pr
12	515	98.3	730	5	AAO17360 Human ela
13	515	98.3	730	8	ADQ19747 Human sof
14	515	98.3	731	3	AAY69068 Amino aci
15	515	98.3	731	4	AAB66657 Human ela
16	515	98.3	731	6	ABU08725 Human ela
17	515	98.3	731	7	ABG75223 Human tro
18	515	98.3	731	7	ABG75223 Human tro
19	515	98.3	757	7	ADP65160 Human ela
20	448	85.5	559	8	ADQ66215 Novel hum
21	448	85.5	617	8	ADB64761 Human pro
22	375.5	71.7	472	4	AAB88422 Human mem
23	351	67.0	870	8	ADQ65871 Novel hum
24	347	66.2	870	7	ADQ65871 Novel hum
25	334.5	63.8	663	7	ADM03792 Human pro

ALIGNMENTS

26	326.5	62.3	864	7	ADP56670 Rat Prote
27	267.5	51.0	660	2	AAY01303 Human tro
28	201.5	38.5	91	5	AAY91258 Nucleic a
29	177.5	33.9	479	2	AAW49739 Protein p
30	174	33.2	832	2	AAR80252 Polymer S
31	174	33.2	832	5	ABP53473 Protein p
32	174	33.2	936	2	AAW09221 SELPDK-CS
33	174	33.2	936	3	AAW51891 Plasmid p
34	174	33.2	936	5	ABG31421 SELPDK-CS
35	174	33.2	936	7	ABW01637 Plasmid p
36	174	33.2	937	2	AAW53547 Amino aci
37	173	33.0	312	5	ABP53480 Protein p
38	173	33.0	378	2	AAW09219 SELPDK po
39	173	33.0	378	2	AAW53545 Amino aci
40	173	33.0	378	5	AAW51889 Plasmid p
41	173	33.0	378	5	ABG31419 SELPDK pr
42	173	33.0	378	7	ABW01635 Plasmid p
43	173	33.0	936	2	AAR80251 Polymer S
44	173	33.0	936	5	ABP53472 Protein p
45	173	33.0	1002	2	AAW09218 SELPDK po

RESULT 1
ID AAR56653 standard; protein; 733 AA.
AC AAR56653;
XX
XX
DT 25-MAR-2003 (revised)
DT 22-MAR-1995 (first entry)
XX
XX
DE Synthetic human tropoelastin (SHEL).

KM Tropoelastin; pharmaceutical; surgical dressing.

XX Synthetic.

XX WO9414958-A1.

XX PD 07-JUL-1994.

XX PF 16-DEC-1993; 93WO-AU000655.

XX PR 22-DEC-1992; 92AU-00006520.

XX PR 28-JUN-1993; 93AU-00009661.

XX PA (UNSY) UNIV SYDNEY.

XX PI Weiss AS, Martin SL;

XX DR WPI: 1994-263633/32.

XX DR N-PSDB; AAQ70941.

XX PT Synthetic polynucleotide(s) - encode recombinant tropoelastins and

1 SMGVPALPGVPGVFPVPGAGLGGALPGCKELKPVPGLAGLGAIGAFPA 60

Db 1 SMGGVPGALPGGVPGGVFGYFGAGLGGALGPGGKPLKPVPGGLAGAGLGAFFPA 60
 QY 61 VTFFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100
 Db 61 VTFFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100

RESULT 2

AAV01301
 ID AAV01301 standard; protein; 733 AA.

AC AAV01301;

DT 07-JUN-1999 (first entry)

DE Amino acid sequence of synthetic human tropoelastin SHEL.

XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
 KM hand lotion; surgical implant; industrial product; human; SHEL.

OS Synthetic.

OS Homo sapiens.

PN MO9903886-A1.

PD 28-JAN-1999.

PF 17-JUL-1998; 98WO-AU000564.

PR 18-JUL-1997; 97AU-00008117.

PA (UNSY) UNIV SYDNEY.

PI Weiss AS;

DR MPI; 1999-132162/11.

DR N-PsDB; AAX27704.

PT New derivatives of human tropoelastin - with elastin-like or
 PT macromolecular binding properties, useful e.g. as surgical implants.

PS Disclosure; Fig 1; 82pp; English.

CC The invention relates to a derivative or variant of human tropoelastin
 CC (hTE) having elastin-like and/or macromolecule (specifically
 CC glycosaminoglycan (GAG)-binding properties. Cells containing vectors
 CC comprising the nucleic acids encoding the variants or derivatives are
 CC used to produce the proteins recombinantly. The tropoelastin derivatives
 CC or hybrid proteins containing the derivatives are useful in medical,
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial
 CC products. The hybrid protein have controllable GAG-binding properties,
 CC depending on presence or absence of a specific fragment, designated
 CC peptide 26A, from hTE. The present sequence represents the amino acid
 CC sequence of the synthetic human tropoelastin SHEL

XX Sequence 733 AA;

Query Match 100.0%; Score 524; DB 2; Length 733;

Best Local Similarity 100.0%; Pred. No. 7.1e-36;

Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SMGGVPGALPGGVPGGVFGYFGAGLGGALGPGGKPLKPVPGGLAGAGLGAFFPA 60

Db 1 SMGGVPGALPGGVPGGVFGYFGAGLGGALGPGGKPLKPVPGGLAGAGLGAFFPA 60

QY 61 VTFFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100

Db 61 VTFFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100

RESULT 3
 ID AAV69135
 AA69135 standard; protein; 515 AA.

AC AAV69135;

DT 30-MAY-2000 (first entry)

DE Amino acid sequence of a human tropoelastin derivative.

XX Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
 KM peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.

OS Homo sapiens.

PN WO200004043-A1.

PD 27-JAN-2000.

PF 19-JUL-1999; 99WO-AU000580.

PR 17-JUL-1998; 98AU-00004723.

PA (UNSY) UNIV SYDNEY.

PI Weiss AS;

DR MPI; 2000-182399/16.

PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
 PT cell growth.

PS Disclosure; Page 131-133; 136pp; English.

CC The present sequence represents a human tropoelastin derivative, which is
 CC representative of tropoelastin derivatives of the invention. In the
 CC tropoelastin derivatives of the invention a subsequence has been mutated
 CC so that susceptibility to proteolysis is reduced or eliminated, or a
 CC subsequence has been inserted so that susceptibility to proteolysis is
 CC increased. The derivatives have with reduced susceptibility, and can be
 CC used where the wild-type protein would be degraded too easily, e.g. in
 CC contact with serum or wound exudate. The tropoelastin derivatives provide
 CC competitive inhibition of protease activity. The tropoelastin
 CC derivatives, and other polypeptides containing tropoelastin derivative-
 CC derived protease-susceptibility sites, are useful in human or veterinary
 CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents
 CC and for inducing chemotaxis. They are also useful for proliferation or
 CC growth inhibition, particularly of smooth muscle cells, epithelial or
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin
 CC derivatives are competitive inhibitors of the protease, and are used for
 CC protecting against lung damage caused by elastin, for inhibiting or
 CC controlling localized growth of cancers or metastases, or to limit
 CC protease activity that causes blood clotting

XX Sequence 515 AA;

Query Match 98.3%; Score 515; DB 3; Length 515;

Best Local Similarity 100.0%; Pred. No. 2.9e-35;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGALPGGVPGGVFGYFGAGLGGALGPGGKPLKPVPGGLAGAGLGAFFPAVT 62

Db 1 GGVPGALPGGVPGGVFGYFGAGLGGALGPGGKPLKPVPGGLAGAGLGAFFPAVT 60

QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100

Db 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 98

RESULT 4

AAV69071

ID AAY69071 standard; protein; 571 AA.
XX
AC AAY69071;
XX
DT 30-MAY-2000 (first entry)
XX
DE Amino acid sequence of a human tropoelastin derivative.
XX
KW Tropoelastin; derivative; proteolysis; protease; antiwinkle;
KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
XX
OS Homo sapiens.
XX
PN WO200004043-A1.
XX
PD 27-JAN-2000.
XX
PF 19-JUL-1999; 99MO-AU000580.
XX
PR 17-JUL-1998; 98AU-00004723.
XX
PA (UNSY) UNIV SYDNEY.
XX
PI Weiss AS;
XX
DR MPI; 2000-182399/16.
XX
PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
PT cell growth.
XX
PS Disclosure; Page 115-117, 136pp; English.
XX
XX The present sequence represents a human tropoelastin derivative, which is
CC representative of tropoelastin derivatives of the invention. In the
CC tropoelastin derivatives of the invention a subsequence has been mutated
CC so that susceptibility to proteolysis is reduced or eliminated, or a
CC subsequence has been inserted so that susceptibility to proteolysis is
CC increased. The derivatives have with reduced susceptibility, and can be
CC used where the wild-type protein would be degraded too easily, e.g. in
CC contact with serum or wound exudate. The tropoelastin derivatives provide
CC competitive inhibition of protease activity. The tropoelastin
CC derivatives, and other polypeptides containing tropoelastin derivative-
CC derived protease-susceptibility sites, are useful in human or veterinary
CC medicine, cosmetics (e.g. antiwinkle or hand lotions), as bulking agents
CC and for inducing chemotaxis. They are also useful for proliferation or
CC growth inhibition, particularly of smooth muscle cells, epithelial or
CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.
CC Peptidomimetics that mimic the protease cleavage site in tropoelastin
CC derivatives are competitive inhibitors of the protease, and are used for
CC protecting against lung damage caused by elastin, for inhibiting or
CC controlling localized growth of cancers or metastases, or to limit
CC protease activity that causes blood clotting
XX
SQ Sequence 571 AA:
XX
XX Query Match 98.3%; Score 515; DB 3; length 571;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-35;
XX Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 3 GGVPGALPGGVPGGVFPFGAGLGLGAGLGGGALGPGGKPLKPPVPGIAGAGLGLGAFPAVT 62
DB 1 GGVPGALPGGVPGGVFPFGAGLGLGAGLGGGALGPGGKPLKPPVPGIAGAGLGLGAFPAVT 60
OY 63 FPGALVPGVADAAAAYKAAKAGAGLGGVPGVGLIGVS 100
DB 61 FPGALVPGVADAAAAYKAAKAGAGLGGVPGVGLIGVS 98

AC ADE40134;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human NOV16b protein - SEQ ID 40.
XX
KW NOVX; cardiant; antiarteriosclerotic; hypotensive; cyostatic; anorectic;
KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
KW antiparkinsonian; antiaesthetic; gynaecological; cardiomyopathy;
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;
KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;
KW tissue typing; human; NOV.
XX
XX Homo sapiens.
XX
PN WO2003064589-A2.
XX
PD 07-AUG-2003.
XX
PF 02-AUG-2002; 2002MO-US024483.
XX
PR 02-AUG-2001; 2001US-0309501P.
PR 03-AUG-2001; 2001US-0310291P.
PR 07-AUG-2001; 2001US-0310544P.
PR 08-AUG-2001; 2001US-0310951P.
PR 09-AUG-2001; 2001US-0311292P.
PR 13-AUG-2001; 2001US-0311979P.
PR 16-AUG-2001; 2001US-0312892P.
PR 17-AUG-2001; 2001US-0313012P.
PR 17-AUG-2001; 2001US-0313415P.
PR 20-AUG-2001; 2001US-0313643P.
PR 20-AUG-2001; 2001US-0313702P.
PR 21-AUG-2001; 2001US-0314031P.
PR 23-AUG-2001; 2001US-0314466P.
PR 28-AUG-2001; 2001US-0315403P.
PR 29-AUG-2001; 2001US-0315853P.
PR 17-SEP-2001; 2001US-0322716P.
PR 21-SEP-2001; 2001US-0323994P.
PR 14-DEC-2001; 2001US-0340233P.
PR 05-FEB-2002; 2002US-0354591P.
PR 19-FEB-2002; 2002US-035478P.
PR 19-APR-2002; 2002US-0373814P.
PR 19-APR-2002; 2002US-0373825P.
PR 19-APR-2002; 2002US-0373989P.
PR 23-APR-2002; 2002US-0374632P.
PR 07-JUN-2002; 2002US-0386971P.
PR 01-AUG-2002; 2002US-00210172.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Kekuda R, Miller CE, Paturajan M, Pena CE, Rieger DK;
PI Shimkets RA, Zerhusen BD, Li L, Ji W, Padigan M, Casman SJ;
PI Voss EZ, Boldog FI, Gorman L, Leite MW, Vernat CM, Anderson DW;
PI Guo X, Zhong M, Gerlach VL, Hjalte T, Rastelli L, Szytek KA;
PI Edinger SR, Ellerman K, Malyanar UM, Machedugali JR, Stone DJ;
PI Alsbobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
PI Sultison G;
XX
XX MPI; 2003-663472/62.
XX
DR N-PSDB; ADE40133.
XX
DR New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; SEQ ID NO 40; 560pp; English.
XX
XX The invention relates to a novel NOVX polypeptide. The polypeptide of the
CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,
CC cyostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,
CC neuroprotective, nootropic, antiparkinsonian, antiaesthetic and

CC gynaecological activities and may be useful in diagnosing, treating or
 CC preventing NOXV-associated disorders including cardiomyopathy,
 CC atherosclerosis, hypertension, cancer, obesity, diabetes AIDS, multiple
 CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's
 CC disease, asthma or fertility disorders. Furthermore, the polypeptides may
 CC be utilised as vaccines whilst the nucleic acids may be used as
 CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,
 CC preventive medicine and pharmacogenomics. The current sequence is that of
 CC the human NOV protein of the invention.

XX SQ Sequence 692 AA;

Query Match 98.3%; Score 515; DB 7; Length 692;

Best Local Similarity 100.0%; Pred. No. 3.8e-35;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIPEGVPGVFFYPGAGIGALGGALGPGGKPLKVPVPGLAGAGIGAFPAVT 62
 DB 27 GGVPGAIPEGVPGVFFYPGAGIGALGGALGPGGKPLKVPVPGLAGAGIGAFPAVT 86
 QY 63 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 100
 DB 87 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 124

RESULT 6

AAV01302 standard; protein; 698 AA.

XX AAV01302;

XX 07-JUN-1999 (first entry)

DE Human tropoelastin variant SHELDelta26A.

XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
 KW hand lotion; surgical implant; industrial product; human; SHELD; variant.

OS Homo sapiens.
 OS Synthetic.

XX WO9303886-A1.

XX 28-JAN-1999.

XX PF 17-JUL-1998; 98WO-AU000564.

XX PR 18-JUL-1997; 97AU-00008117.

XX PA (UNSY) UNIV SYDNEY.

XX PI Weiss AS;

XX WPI; 1999-132162/11.

PT New derivatives of human tropoelastin - with elastin-like or
 PT macromolecular binding properties, useful e.g. as surgical implants.

XX Claim 13; Fig 2; 82pp; English.

CC The invention relates to a derivative or variant of human tropoelastin
 CC (hTE) having elastin-like and/or macromolecule (specifically
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
 CC comprising the nucleic acids encoding the variants or derivatives are
 CC used to produce the proteins recombinantly. The tropoelastin derivatives
 CC or hybrid proteins containing the derivatives are useful in medical,
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial
 CC products. The hybrid protein have controllable GAG-binding properties,
 CC depending on presence or absence of a specific fragment, designated
 CC peptide 26A, from hTE. The present sequence represents the synthetic
 CC human tropoelastin variant SHELDelta26A

XX SQ Sequence 698 AA;

Query Match 98.3%; Score 515; DB 2; Length 698;

Best Local Similarity 100.0%; Pred. No. 3.9e-35;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIPEGVPGVFFYPGAGIGALGGALGPGGKPLKVPVPGLAGAGIGAFPAVT 62
 DB 1 GGVPGAIPEGVPGVFFYPGAGIGALGGALGPGGKPLKVPVPGLAGAGIGAFPAVT 60
 QY 63 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 100
 DB 61 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 98

RESULT 7

AAV69069 standard; protein; 698 AA.

XX AAV69069;

XX 30-MAY-2000 (first entry)

DE Amino acid sequence of a human reduced tropoelastin derivative.

XX Tropoelastin; derivative; SHELDelta-26A; SHELD; proteolysis; protease;
 KW anti-wrinkle; hand lotion; bulking agent; chemotaxis; proliferation;
 KW growth inhibition; peptidomimetic; lung damage; elastin; cancer;
 KW metastasis; blood clotting.

OS Synthetic.

OS Homo sapiens.

XX WO200004043-A1.

XX 27-JAN-2000.

XX PF 19-JUL-1999; 99WO-AU000580.

XX PR 17-JUL-1998; 98AU-00004723.

XX PA (UNSY) UNIV SYDNEY.

XX PI Weiss AS;

XX WPI; 2000-182399/16.

XX DR N-PSDB, AA261144.

XX PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
 XX cell growth.

XX Disclosure; Page 110-112; 136pp; English.

CC The present sequence represents a human reduced tropoelastin derivative,
 CC designated SHELDelta-26A. The sequence is produced by removing exon 26a
 CC of SHELD (SHELD not defined). The protein is representative of tropoelastin
 CC derivatives of the invention, in which a subsequence has been mutated so
 CC that susceptibility to proteolysis is reduced or eliminated, or a
 CC subsequence has been inserted so that susceptibility to proteolysis is
 CC increased. The derivatives have with reduced susceptibility, and can be
 CC used where the wild-type protein would be degraded too easily, e.g. in
 CC contact with serum or wound exudate. The tropoelastin derivatives provide
 CC competitive inhibition of protease activity. The tropoelastin
 CC derivatives, and other polypeptides containing tropoelastin derivative-
 CC derived protease-susceptibility sites, are useful in human or veterinary
 CC medicine, cosmetics (e.g. anti-wrinkle or hand lotions), as bulking agents
 CC and for inducing chemotaxis. They are also useful for proliferation or
 CC growth inhibition, particularly of smooth muscle cells, epithelial or
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin
 CC derivatives are competitive inhibitors of the protease, and are used for
 CC protecting against lung damage caused by elastin, for inhibiting or

CC controlling localized growth of cancers or metastases, or to limit
CC protease activity that causes blood clotting
XX
SQ Sequence 698 AA;

Query Match 98.3%; Score 515; DB 3; Length 698;
Best Local Similarity 100.0%; Pred. No. 3.9e-35;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GGVPGAIPGVPFGVFPAGLGGALGGALPGGKPLKVPVGGIAGAGLGAFAFPAVT 62
DB 1 GGVPGAIPGVPFGVFPAGLGGALGGALPGGKPLKVPVGGIAGAGLGAFAFPAVT 60
OY 63 FPGALVPGGVADAAAAYKAKAGAGLGGVPGVGGIGVS 100
DB 61 FPGALVPGGVADAAAAYKAKAGAGLGGVPGVGGIGVS 98

RESULT 8
ADE40132
ID ADE40132 standard; protein; 711 AA.
XX

AC ADE40132;

DT 29-JAN-2004 (first entry)

DE Human NOV16a protein - SEQ ID 38.

XX NOVX: cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
KW antiparkinsonian; antiaesthetic; gynaecological; cardiomyopathy;
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;
KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;
XX tissue typing; human; NOV.

OS Homo sapiens.

PN WO2003064589-A2.

PD 07-AUG-2003.

PF 02-AUG-2002; 2002WO-US024483.

XX 02-AUG-2001; 2001US-0309501P.
PR 03-AUG-2001; 2001US-0310291P.
PR 07-AUG-2001; 2001US-0310544P.
PR 08-AUG-2001; 2001US-0310951P.
PR 09-AUG-2001; 2001US-0311292P.
PR 13-AUG-2001; 2001US-0311979P.
PR 16-AUG-2001; 2001US-0312892P.
PR 17-AUG-2001; 2001US-0313201P.
PR 17-AUG-2001; 2001US-0313415P.
PR 20-AUG-2001; 2001US-0313643P.
PR 20-AUG-2001; 2001US-0313702P.
PR 21-AUG-2001; 2001US-0314031P.
PR 23-AUG-2001; 2001US-0314466P.
PR 28-AUG-2001; 2001US-0315403P.
PR 29-AUG-2001; 2001US-0315853P.
PR 17-SEP-2001; 2001US-0322716P.
PR 21-SEP-2001; 2001US-0323994P.
PR 14-DEC-2001; 2001US-0340233P.
PR 05-FEB-2002; 2002US-0354591P.
PR 19-MAR-2002; 2002US-0365478P.
PR 19-APR-2002; 2002US-0373814P.
PR 19-APR-2002; 2002US-0373825P.
PR 19-APR-2002; 2002US-0373989P.
PR 23-APR-2002; 2002US-0374632P.
PR 07-JUN-2002; 2002US-0386971P.
PR 01-AUG-2002; 2002US-00210172.

XX (CURA-) CURAGEN CORP.

PI Kekuda R, Miller CE, Patturajan M, Pena CE, Rieger DK;
PI Shimkets RA, Zernhusen BD, Li L, Ji W, Padigaru M, Casman SJ;
PI Voss EZ, Boldog FU, Gotman L, Leite MW, Vernet CAM, Anderson DW;
PI Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;
PI Balingier SR, Ellerman K, Malyankar UM, Macdonald JR, Stone DJ;
PI Alsbrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
PI Smithson G;

DR WPI, 2003-663472/62.
DR N-PSDB; ADE40131.

XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.

PS Claim 1; SEQ ID NO 38; 560bp; English.

XX The invention relates to a novel NOVX polypeptide. The polypeptide of the
CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,
CC cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,
CC neuroprotective, nootropic, antiparkinsonian, antiaesthetic and
CC gynaecological activities and may be useful in diagnosing, treating or
CC preventing NOVX-associated disorders including cardiomyopathy,
CC atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple
CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's
CC disease, asthma or fertility disorders. Furthermore, the polypeptides may
CC be utilised as vaccines whilst the nucleic acids may be used as
CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,
CC preventive medicine and pharmacogenomics. The current sequence is that of
CC the human NOV protein of the invention.

SQ Sequence 711 AA;

Query Match 98.3%; Score 515; DB 7; Length 711;
Best Local Similarity 100.0%; Pred. No. 3.9e-35;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GGVPGAIPGVPFGVFPAGLGGALGGALPGGKPLKVPVGGIAGAGLGAFAFPAVT 62
DB 27 GGVPGAIPGVPFGVFPAGLGGALGGALPGGKPLKVPVGGIAGAGLGAFAFPAVT 86

OY 63 FPGALVPGGVADAAAAYKAKAGAGLGGVPGVGGIGVS 100
DB 87 FPGALVPGGVADAAAAYKAKAGAGLGGVPGVGGIGVS 124

RESULT 9

ID AAB08630 standard; peptide; 712 AA.

XX AAB08630;

DT 20-DEC-2000 (first entry)

DE Amino acid sequence of a human elastin polypeptide.

XX Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
KW smooth muscle cell differentiation; smooth muscle cell migration;
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
KW SVAS; hypertension; transplant arteriopathy.

OS Homo sapiens.

PN WO200050068-A2.

PD 31-AUG-2000.

PF 28-FEB-2000; 2000WO-US002526.

PR 26-FEB-1999; 99US-00258217.

PA (UTAH) UNIV UTAH RES FOUND.
XX
XX Keating MT, Li DY;
XX
XX WPI; 2000-533134/48.
DR
XX
XX Elastin based compositions useful for treating atherosclerosis,
PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,
PT aneurysm, dissection SVAS and/or hypertension.
XX
XX
PS Example 3; Page 46; 79pp; English.
XX
XX The present sequence represents a human elastin. Peptides derived from
CC elastin are used in compositions of the invention. The specification
CC describes elastin based compositions that are potent regulators of smooth
CC muscle cell proliferation, differentiation and migration in vivo. The
CC elastin-based compositions comprise at least one elastic fibre, elastins,
CC tropoelastins (or fragments of them) which have biological activities
CC comprising: inhibiting the proliferation of smooth muscle cells in vivo;
CC stimulating the differentiation of smooth muscle cell in vivo; and
CC regulating the migration of smooth muscle cells in vivo. The compositions
CC may be used for the prophylaxis or treatment of a disorder characterized
CC by diminished capacity to regulate smooth muscle cell function such as
CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant
CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated
CC also include SVAS (undefined), hypertension, and transplant arteriopathy
XX
SQ Sequence 712 AA;
XX
Query Match 98.3%; Score 515; DB 3; Length 712;
Best Local Similarity 100.0%; Pred. No. 3.9e-35;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 3 GGVPGAIPEGVPGVGYPPGAGLGGGALGPGKPLKVPGLAGAGLGAAPAVT 62
|||
DB 27 GGVPGAIPEGVPGVGYPPGAGLGGGALGPGKPLKVPGLAGAGLGAAPAVT 86
|||
QY 63 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 100
|||
DB 87 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 124
|||
XX
RESULT 10
AAW46315
ID AAW46315 standard; protein; 730 AA.
XX
AC AAW46315;
XX
DT 23-JUL-1998 (first entry)
XX
DE Human elastin containing non-natural polypeptide MFU-1 sequence.
XX
KW MFU-1; minimal functional unit; elastin; human; fibrous protein;
KW beta-sheet; coating; wound dressing.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 374..499
FT /note="MFU-1 polypeptide"
XX
XX MO9805685-A2.
XX
XX 12-FEB-1998.
XX
XX 07-AUG-1997; 97WO-CA000560.
XX
XX 07-AUG-1996; 96US-0023552P.
XX
XX 07-AUG-1997; 97US-00911364.
XX
XX (PROT-) PROTEIN SPECIALTIES LTD.
XX (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX

PI Rothstein A, Keeley FW, Rothstein SJ;
XX
XX WPI; 1998-145551/13.
DR
XX
XX New non-natural polypeptide with multiple beta-sheet, beta-turn
PT structures - particularly based on human elastin, useful for coating
PT prostheses, as wound dressings, etc., allows ingrowth of cells.
XX
XX Claim 5; Fig 1B; 39pp; English.
XX
XX This represents the human elastin sequence containing the minimal
CC functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a
CC polypeptide that has at least 3 beta-sheet/ beta-turn structures, but is
CC not a naturally occurring fibrous protein. Each beta-sheet structure has
CC 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at
CC least 1 amino acid that can take part in crosslinking. The polypeptide
CC can also be derived from the sequences of animal elastin, lampirin and
CC spider silk protein. The MFU polypeptides are self-aligning peptides
CC having the same primary structure as part of a natural fibrous protein.
CC They are used to coat prostheses made of animal or synthetic material or
CC metal, particularly for use as blood vessel or heart valve replacements,
CC wound or burn dressings, or stents. They can be used in cosmetic, elastic
CC or high-tensile strength materials, e.g. ropes or parachute cord.
CC Prostheses based on the MFU allow penetration of endothelial cells, so
CC become permanent, living, tissue replacements. The MFU polypeptides have
CC better biocompatibility than known elastin-based materials. They are well
CC defined, homogeneous material and are easier to manipulate and produce
CC than full-length elastins. They are non-thrombogenic and non-immunogenic.
CC Materials can be made from 2 or more different MFU polypeptides to allow
CC properties to be tailored for particular applications, e.g. combining the
CC high extensibility of elastin and the high tensile strength of spider
XX silk protein
XX
SQ Sequence 730 AA;
XX
Query Match 98.3%; Score 515; DB 2; Length 730;
Best Local Similarity 100.0%; Pred. No. 4e-35;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 3 GGVPGAIPEGVPGVGYPPGAGLGGGALGPGKPLKVPGLAGAGLGAAPAVT 62
|||
DB 1 GGVPGAIPEGVPGVGYPPGAGLGGGALGPGKPLKVPGLAGAGLGAAPAVT 60
|||
QY 63 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 100
|||
DB 61 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 98
|||
XX
RESULT 11
AAB08631
ID AAB08631 standard; peptide; 730 AA.
XX
AC AAB08631;
XX
DT 20-DEC-2000 (first entry)
XX
DE Fusion protein comprising human elastin and c-myc.
XX
XX
KW Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
KW smooth muscle cell differentiation; smooth muscle cell migration;
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
KW SVAS; hypertension; transplant arteriopathy.
XX
XX Synthetic.
XX Homo sapiens.
XX Unidentified.
XX
XX MO200050068-A2.
XX
XX 31-AUG-2000.
XX
XX 28-FEB-2000; 2000WO-US002526.
XX
XX

XX 26-FEB-1999; 99US-00258217.
XX (UTAH) UNIV UTAH RES FOUND.
XX Keating MT, Li DY;
XX WPI; 2000-533134/48.
XX
XX Elastin based compositions useful for treating atherosclerosis,
XX PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,
XX PT aneurysm, dissection SVAS and/or hypertension.
XX
XX Example 3; Page 48; 79pp; English.
XX
XX The present sequence represents a fusion protein, comprising human
XX CC elastin and c-myc, preceded by a His tag. The protein is used in
XX CC compositions of the invention. The specification describes elastin based
XX CC compositions that are potent regulators of smooth muscle cell
XX CC proliferation, differentiation and migration in vivo. The elastin-based
XX CC compositions comprise at least one elastic fibre, elastins, tropoelastins
XX CC (or fragments of them) which have biological activities comprising:
XX CC inhibiting the proliferation of smooth muscle cells in vivo; stimulating
XX CC the differentiation of smooth muscle cell in vivo; and regulating the
XX CC migration of smooth muscle cells in vivo. The compositions may be used
XX CC for the prophylaxis or treatment of a disorder characterized by
XX CC diminished capacity to regulate smooth muscle cell function such as
XX CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant
XX CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated
XX CC also include SVAS (undefined), hypertension, and transplant arteriopathy
XX
SQ Sequence 730 AA;

Query Match 98.3%; Score 515; DB 3; Length 730;
Best Local Similarity 100.0%; Pred. No. 4e-35;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGALPGGVPGGVPPGAGLGLAGLGGALGPGGKPLKVPVPGLAGLGLAGLGAFAFPAVT 62
DB 36 GGVPGALPGGVPPGAGLGLAGLGGALGPGGKPLKVPVPGLAGLGLAGLGAFAFPAVT 95

QY 63 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 100
DB 96 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 133

RESULT 12

AAO17360 standard; protein; 730 AA.

AC AAO17360;

DT 19-JUL-2002 (first entry)

DE Human elastin.

XX Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;
XX KM aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;
XX KM insulin-like growth factor binding protein-2; alpha-2 type IV collagen;
XX KM transmembrane receptor PTK7; collagen type XVIII alpha 1;
XX KM platelet derived growth factor receptor alpha; laminin M chain;
XX KM subtilisin like protein PACE4; nidogen.

XX Homo sapiens.

OS Homo sapiens.

PN EPI191107-A2.

PD 27-MAR-2002.

PF 21-AUG-2001; 2001EP-00250300.

PT 25-SEP-2000; 2000DE-01048633.

PA (SCHD) SCHERING AG.
XX Hess-Stump H, Haendler B, Kraetzschmar J, Krefz B, Winterhager B;
XX PI Regidor P, Scotti S;
XX WPI; 2002-317413/36.
XX
XX In vitro diagnosis and monitoring of endometriosis, comprises detecting
XX PT reduced expression of specific gene products, e.g. from the fibronectin
XX PT gene.
XX
XX Claim 1; Page 15-16; 21pp; German.
XX
XX The present invention relates to a method for the in vitro diagnosis of
XX CC endometriosis by determining the amount of gene product from at least one
XX CC specific gene in a patient sample and comparing this with the amount of
XX CC gene product in a control sample. A reduced level is indicative of
XX CC endometriosis. The gene products may be fibronectin, p27, reticulocalbin,
XX CC aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,
XX CC insulin-like growth factor binding protein-2, alpha-2 type IV collagen,
XX CC transmembrane receptor PTK7, collagen type XVIII alpha 1, platelet
XX CC derived growth factor receptor alpha, laminin M chain, subtilisin like
XX CC protein PACE4 or nidogen. The method is useful for initial diagnosis of
XX CC endometriosis, and also for monitoring progress and treatment of the
XX CC disease. The present sequence is human elastin
XX
SQ Sequence 730 AA;

Query Match 98.3%; Score 515; DB 5; Length 730;
Best Local Similarity 100.0%; Pred. No. 4e-35;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGALPGGVPGGVPPGAGLGLAGLGGALGPGGKPLKVPVPGLAGLGLAGLGAFAFPAVT 62
DB 27 GGVPGALPGGVPPGAGLGLAGLGGALGPGGKPLKVPVPGLAGLGLAGLGAFAFPAVT 86

QY 63 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 100
DB 87 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 124

RESULT 13

ADQ19747 standard; protein; 730 AA.

AC ADQ19747;

DT 26-AUG-2004 (first entry)

DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.

XX soft tissue sarcoma; cytoskeletal; gene therapy; vaccine; screening; human.

XX Homo sapiens.

PN WO2004048938-A2.

PD 10-JUN-2004.

PF 26-NOV-2003; 2003WO-US038193.

PR 26-NOV-2002; 2002US-0429739P.

PA (PROT-) PROTEIN DESIGN LABS INC.

PI Aziz N, Ginsburg WM, Zlotnick A;

PD WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression
XX PT of a gene in a first soft tissue sample and a normal soft tissue sample
XX PT and comparing the gene expression, also useful in treating soft tissue
XX PT sarcoma.

PS Disclosure; Page 107-109; 136bp; English.

CC elastin polypeptide. This protein is useful in a cosmetic material or a

CC prosthetic material such as prosthesis for blood vessel replacements, for
CC heart valve replacement, tissue replacement, for covering burns, for
CC covering wounds and stents
XX
SQ Sequence 731 AA;

Query Match 98.3%; Score 515; DB 4; Length 731;
Best Local Similarity 100.0%; Pred. No. 4e-35; Indels 0; Gaps 0;
Matches 98; Conservative 0; Mismatches 0;

QY 3 GGVPGAIPGGVPGGFYPPGAGLGGALGGALPGGKPLKVPYGGIAGAGLGAFFPAVT 62
DB 1 GGVPGAIPGGVPGGFYPPGAGLGGALGGALPGGKPLKVPYGGIAGAGLGAFFPAVT 60
QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGIGVS 100
DB 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGIGVS 98

Search completed: August 10, 2005, 07:33:50
Job time : 121.905 secs

THIS PAGE IS BLANK

GenCore Version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2005, 07:27:07 ; Search time 29.8507 Seconds
(without alignments)
250.074 Million cell updates/sec

Title: US-09-743-818A-4_COPY_1_100

Perfect score: 524
Sequence: 1 SMGVPGALPGVPGVFPV.....AAKAGLGVPVGLGLGS 100

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	524	100.0	733	3	US-08-464-700-2
2	515	98.3	730	4	US-09-961-403-8
3	515	98.3	731	2	US-08-911-364-1
4	515	98.3	731	4	US-09-340-736E-1
5	515	98.3	731	4	US-09-964-662-1
6	515	98.3	732	2	US-08-678-039A-40
7	177.5	33.9	479	1	US-08-397-633A-78
8	174	33.2	832	1	US-08-212-237-4
9	174	33.2	832	3	US-08-806-029-27
10	174	33.2	832	5	PCT-US95-02772-4
11	174	33.2	936	2	US-08-707-237A-108
12	174	33.2	936	4	US-08-642-246-30
13	174	33.2	936	3	US-09-451-206-30
14	174	33.2	936	5	PCT-US96-06229-30
15	173	33.0	312	3	US-08-806-029-34
16	173	33.0	378	2	US-08-707-237A-104
17	173	33.0	378	3	US-08-642-246-26
18	173	33.0	378	4	US-09-451-206-26
19	173	33.0	378	5	PCT-US96-06229-26
20	173	33.0	936	1	US-08-212-237-3
21	173	33.0	936	3	US-08-806-029-26
22	173	33.0	936	5	PCT-US95-02772-3
23	173	33.0	1002	2	US-08-707-237A-103
24	173	33.0	1002	3	US-08-642-246-25
25	173	33.0	1002	4	US-09-451-206-25
26	173	33.0	1002	5	PCT-US96-06229-25
27	172	32.8	486	1	US-08-397-633A-77

28	171	32.6	262	1	US-08-397-633A-73	Sequence 73, Appl
29	168	32.1	696	3	US-08-806-029-36	Sequence 36, Appl
30	168	32.1	750	3	US-08-806-029-25	Sequence 25, Appl
31	167.5	32.0	251	1	US-08-397-633A-74	Sequence 74, Appl
32	166	31.7	1413	1	US-08-175-155-39	Sequence 39, Appl
33	166	31.7	1413	2	US-08-707-237A-45	Sequence 45, Appl
34	166	31.7	1464	3	US-08-477-509B-74	Sequence 74, Appl
35	166	31.7	1464	3	US-08-482-085B-74	Sequence 74, Appl
36	166	31.7	1465	3	US-09-444-791A-74	Sequence 74, Appl
37	164	31.3	988	3	US-08-212-237-5	Sequence 5, Appl
38	164	31.3	988	3	US-08-806-029-28	Sequence 28, Appl
39	164	31.3	988	5	PCT-US95-02772-5	Sequence 5, Appl
40	162.5	31.0	287	1	US-08-397-633A-76	Sequence 76, Appl
41	162	30.9	281	1	US-08-397-633A-75	Sequence 75, Appl
42	161.5	30.8	768	3	US-08-806-029-35	Sequence 35, Appl
43	161.5	30.8	877	1	US-08-397-633A-54	Sequence 54, Appl
44	161.5	30.8	884	1	US-08-397-633A-68	Sequence 68, Appl
45	161.5	30.8	884	2	US-08-435-641-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-464-700-2
Sequence 2, Application US/08464700
Patent No. 6232458
GENERAL INFORMATION:
APPLICANT: WEISS, ANTHONY S
APPLICANT: MARTIN, STEPHEN L
TITLE OF INVENTION: SYNTHETIC POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,700
FILING DATE: 7-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL6520
FILING DATE: 22-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL9661
FILING DATE: 28-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU93/00655
FILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GHC3USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 733 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-700-2
Query Match 100.0%; Score 524; DB 3; Length 733;

Best Local Similarity 100.0%; Pred. No. 2,3e-38;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SMGVPGAIPEGVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPPA 60

DB 1 SMGVPGAIPEGVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPPA 60

QY 61 VTFPGALVPGVADAAAAYKAAKAGAGLGVPGVGLGVS 100
DB 61 VTFPGALVPGVADAAAAYKAAKAGAGLGVPGVGLGVS 100

RESULT 2

US-09-961-403-8
Sequence 8, Application US/09961403

Patent No. 6780594
GENERAL INFORMATION:
APPLICANT: HE-STUMP, HOLGER
APPLICANT: HAENDLER, BERNARD
APPLICANT: KRAETZSCHMAR, JOERN
APPLICANT: KREFT, BERTHOLT
APPLICANT: WINTERHAGER, ELKE
APPLICANT: REGIDOR, PEDRO
APPLICANT: SCOTTI, SIMONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
FILE REFERENCE: SCH-1789
CURRENT APPLICATION NUMBER: US/09/961,403
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 730
TYPE: PRT
ORGANISM: Homo sapiens
US-09-961-403-8

Query Match 98.3%; Score 515; DB 4; Length 730;
Best Local Similarity 100.0%; Pred. No. 1.4e-37;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIPEGVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPPA 62

DB 27 GGVPGAIPEGVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPPA 86

QY 63 FPGALVPGVADAAAAYKAAKAGAGLGVPGVGLGVS 100
DB 87 FPGALVPGVADAAAAYKAAKAGAGLGVPGVGLGVS 124

RESULT 3

US-08-911-364-1
Sequence 1, Application US/08911364

Patent No. 5969106
GENERAL INFORMATION:
APPLICANT: ROTHSTEIN, ASER
APPLICANT: KEELY, FRED W.
APPLICANT: ROTHSTEIN, STEVEN J.
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN
TITLE OF INVENTION: ELASTIN AND OTHER FIBROUS PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/911,364
FILING DATE: 07-AUG-1997
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,552

FILING DATE: 07-AUG-1996

ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 041082/0104

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 731 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-911-364-1
Query Match 98.3%; Score 515; DB 2; Length 731;
Best Local Similarity 100.0%; Pred. No. 1.4e-37;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIPEGVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPPA 62

DB 1 GGVPGAIPEGVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPPA 60

QY 63 FPGALVPGVADAAAAYKAAKAGAGLGVPGVGLGVS 100
DB 61 FPGALVPGVADAAAAYKAAKAGAGLGVPGVGLGVS 98

RESULT 4

US-09-340-736E-1
Sequence 1, Application US/09340736E

Patent No. 6489446
GENERAL INFORMATION:
APPLICANT: ROTHSTEIN, ASER
APPLICANT: KEELY, FRED
APPLICANT: ROTHSTEIN, STEVEN
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN
TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS
FILE REFERENCE: 041082/0110
CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 08/911,364
PRIOR FILING DATE: 1997-08-07
PRIOR APPLICATION NUMBER: 60/023,552
PRIOR FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 731
TYPE: PRT
ORGANISM: Homo sapiens
US-09-340-736E-1

Query Match 98.3%; Score 515; DB 4; Length 731;
Best Local Similarity 100.0%; Pred. No. 1.4e-37;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIPEGVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPPA 62

DB 1 GGVPGAIPEGVPGVFPFGAGLGGALGPGGKPLKVPVPGLAGAGLAGAPPA 60

QY 63 FPGALVPGVADAAAAYKAAKAGAGLGVPGVGLGVS 100
DB 61 FPGALVPGVADAAAAYKAAKAGAGLGVPGVGLGVS 98

Db 191 GVGVPGVGV 139

```

RESULT 8
US-08-212-237-4
; Sequence 4, Application US/08212237
; Patent No. 5606019
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: Synthetic Proteins As Implantables
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,237
; FILING DATE: 11-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Berttram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58847/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 832 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-212-237-4

Query Match 33.2%; Score 174; DB 1; Length 832;
Best Local Similarity 39.3%; Pred. No. 1.3e-07;
Matches 53; Conservative 6; Mismatches 32; Indels 44; Gaps 7;

QY 4 GVPG-AIPG-GVPG-----GVFPAGALGAGGALPGGKPLKPPVPGIAGAGLGA 57
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 10 GVPGVGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 64
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 58 FPAVTFPGALVPG-----GVADAAAYKA-----AKGA 86
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 VPGVGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 124
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 87 GLGVPGVG--GLGV 99
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 125 GAGSVPGVPGVPGV 139

RESULT 9
US-08-806-029-27
; Sequence 27, Application US/08806029
; Patent No. 6380154
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
; STREET: Delivery and Tissue Augmentation
; CITY:
; STATE:
; COUNTRY:
; ZIP:
; COMPUTER READABLE FORM:
; MEDIUM TYPE:
; OPERATING SYSTEM:
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ADDRESSER: Flehr, Hohbach, Test, Albritton & Herbert
```

```

; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/806,029
; FILING DATE: 24-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,237
; FILING DATE: 11-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Treccartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 832 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
US-08-806-029-27

Query Match 33.2%; Score 174; DB 3; Length 832;
Best Local Similarity 39.3%; Pred. No. 1.3e-07;
Matches 53; Conservative 6; Mismatches 32; Indels 44; Gaps 7;

QY 4 GVPG-AIPG-GVPG-----GVFPAGALGAGGALPGGKPLKPPVPGIAGAGLGA 57
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 10 GVPGVGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 64
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 58 FPAVTFPGALVPG-----GVADAAAYKA-----AKGA 86
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 VPGVGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 124
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 87 GLGVPGVG--GLGV 99
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 125 GAGSVPGVPGVPGV 139
```

```

RESULT 10
PCT-US95-02772-4
; Sequence 4, Application PC/TUS9502772
; GENERAL INFORMATION:
; APPLICANT: Protein Polymer Technologies, Inc.
; TITLE OF INVENTION: Synthetic Proteins As Implantables
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02772
; FILING DATE:
; CLASSIFICATION:
```


Query Match 33.2%; Score 174; DB 4; Length 936;

Qy	GVNGV-AI-PG-GVPG-----GVFYPGAGLGLTGS-----GALPGP-----GK	37
Db	69 GVGKGKGPVGVPVGVPVGVPVGAGASGAAGAAGSGVGPLGGPLGPGVGPVGVPVG	128
Qy	ELTPVPBG-----GLAGAGIGAGLGA-----	57
Db	129 PGKGVPGVGPVGVPVGVPVGPCAGAGASGAAGSAGVGPLGPLGPGVGPVGVPVG	188
Qy	--FPATPPGVALPVGGVDADAAAAAAYAAKAKAGAGLG-----GVPFGV--GLGV	99
Db	189 KGVPGVGPVGVPVGVPVGPCAGAGSAGAGAGSSVGPLGLGPGVGPVGVPVG	244


```
RESULT 15
US-08-806-029-34
; Sequence 34, Application US/08806029
; Patent No. 6380154
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; APPLICANT: Steadronsky, Erwin R.
; TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
; TITLE OF INVENTION: Delivery and Tissue Augmentation
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohnach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/806.029
; FILING DATE: 24-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,237
; FILING DATE: 11-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Treacartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-806-029-34

Query Match          33.0%; Score 173; DB 3; Length 312;
Best Local Similarity 36.1%; Pred. No. 5.9e-08;
Matches 57; Conservative 7; Mismatches 32; Indels 62; Gaps 8;

QY 4 GVPG-AIPG-GVPG-----GVFPAGALGAGALPG-----GKPLKVP 43
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 30 GVPGKGVPGVPGVPGVPGVPGAGAGSAGAGSAGVPGVPGVPGVPGKGV 89
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 44 G-----GLAGGLAGLGA-----FPAVTFPGAL 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 90 GVGVPGVPGVPGVPGAGAGSAGAGSAGVPGVPGVPGVPGVPGKGV 149
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 68 VPGGVADAAAYKAKAGAGL-----GVPGV--GLGV 99
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 150 VPGVPGAGAGSAGAGSAGVPGVPGVPGVPGV 187
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Search completed: August 10, 2005, 07:39:40
Job time : 30.8507 secs

THIS PAGE IS BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd

OM protein - protein search, using sw model

Run on: August 10, 2005, 07:37:53 ; Search time 104.478 Seconds
(without alignments)
373.667 Million cell updates/sec

Title: US-09-743-818A-4_COPY_1_100

Sequence: 1 SMGGVPGAIPGVPGVFP...AAKAGAGLGVPVGGLGS 100

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 1752860

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published Applications AA:*

- 1: /cgn2_6/ptodata1/1/pubppa/US07_PUBCOMB.pdp.*
- 2: /cgn2_6/ptodata1/1/pubppa/PCT_NEW_PUB.pdp.*
- 3: /cgn2_6/ptodata1/1/pubppa/US06_NEW_PUB.pdp.*
- 4: /cgn2_6/ptodata1/1/pubppa/US06_PUBCOMB.pdp.*
- 5: /cgn2_6/ptodata1/1/pubppa/US07_NEW_PUB.pdp.*
- 6: /cgn2_6/ptodata1/1/pubppa/PCU5_PUBCOMB.pdp.*
- 7: /cgn2_6/ptodata1/1/pubppa/US08_NEW_PUB.pdp.*
- 8: /cgn2_6/ptodata1/1/pubppa/US08_PUBCOMB.pdp.*
- 9: /cgn2_6/ptodata1/1/pubppa/US09A_PUBCOMB.pdp.*
- 10: /cgn2_6/ptodata1/1/pubppa/US09C_PUBCOMB.pdp.*
- 11: /cgn2_6/ptodata1/1/pubppa/US09B_PUBCOMB.pdp.*
- 12: /cgn2_6/ptodata1/1/pubppa/US09_NEW_PUB.pdp.*
- 13: /cgn2_6/ptodata1/1/pubppa/US10A_PUBCOMB.pdp.*
- 14: /cgn2_6/ptodata1/1/pubppa/US10B_PUBCOMB.pdp.*
- 15: /cgn2_6/ptodata1/1/pubppa/US10C_PUBCOMB.pdp.*
- 16: /cgn2_6/ptodata1/1/pubppa/US10D_PUBCOMB.pdp.*
- 17: /cgn2_6/ptodata1/1/pubppa/US10E_PUBCOMB.pdp.*
- 18: /cgn2_6/ptodata1/1/pubppa/US10_NEW_PUB.pdp.*
- 19: /cgn2_6/ptodata1/1/pubppa/US11A_PUBCOMB.pdp.*
- 20: /cgn2_6/ptodata1/1/pubppa/US11_NEW_PUB.pdp.*
- 21: /cgn2_6/ptodata1/1/pubppa/US60_NEW_PUB.pdp.*
- 22: /cgn2_6/ptodata1/1/pubppa/US60_PUBCOMB.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB	ID	Description
1	515	98.3	692	15	US-10-210-172-40	Sequence 40, Appl
2	515	98.3	711	15	US-10-210-172-38	Sequence 38, Appl
3	515	98.3	730	10	US-09-961-403-8	Sequence 8, Appl
4	515	98.3	730	16	US-10-723-860-2566	Sequence 2566, Appl
5	515	98.3	731	10	US-09-964-662-1	Sequence 1, Appl
6	515	98.3	788	16	US-10-852-065-4	Sequence 4, Appl
7	515	98.3	788	16	US-10-852-575-3	Sequence 3, Appl
8	448	85.5	617	15	US-10-104-271-2915	Sequence 2915, Appl
9	334.5	63.8	663	15	US-10-108-260A-2477	Sequence 2477, Appl
10	174	33.2	936	14	US-08-806-029-27	Sequence 27, Appl
11	174	33.2	936	14	US-10-117-931-30	Sequence 30, Appl

12	173	33.0	312	8	US-08-806-029-9-1	Sequence 3, Appl
13	173	33.0	378	14	US-10-117-931-26	Sequence 26, Appl
14	173	33.0	936	8	US-08-806-029-26	Sequence 26, Appl
15	173	33.0	1002	14	US-10-117-931-25	Sequence 25, Appl
16	168	32.1	696	8	US-08-806-029-36	Sequence 36, Appl
17	168	32.1	696	15	US-10-441-965-23	Sequence 23, Appl
18	168	32.1	750	8	US-08-806-029-25	Sequence 25, Appl
19	166	31.7	1465	14	US-10-096-986-74	Sequence 74, Appl
20	165.5	31.6	696	15	US-10-441-965-21	Sequence 21, Appl
21	164	31.3	562	16	US-10-720-025-33	Sequence 33, Appl
22	164	31.3	730	16	US-10-720-025-35	Sequence 35, Appl
23	164	31.3	988	8	US-08-806-029-28	Sequence 28, Appl
24	164	31.3	1382	16	US-10-720-025-60	Sequence 60, Appl
25	164	31.3	1550	16	US-10-720-025-54	Sequence 54, Appl
26	163	31.1	450	9	US-09-812-382-6	Sequence 6, Appl
27	161.5	30.8	244	16	US-10-800-179-27	Sequence 27, Appl
28	161.5	30.8	244	16	US-10-845-775A-27	Sequence 27, Appl
29	161.5	30.8	244	16	US-10-845-936A-27	Sequence 27, Appl
30	161.5	30.8	244	16	US-10-939-036-27	Sequence 27, Appl
31	161.5	30.8	246	16	US-10-800-179-26	Sequence 26, Appl
32	161.5	30.8	246	16	US-10-800-179-26	Sequence 26, Appl
33	161.5	30.8	246	16	US-10-845-775A-26	Sequence 26, Appl
34	161.5	30.8	246	16	US-10-845-775A-28	Sequence 28, Appl
35	161.5	30.8	246	16	US-10-845-936A-26	Sequence 26, Appl
36	161.5	30.8	246	16	US-10-845-936A-28	Sequence 28, Appl
37	161.5	30.8	246	18	US-10-939-036-26	Sequence 26, Appl
38	161.5	30.8	246	18	US-10-939-036-28	Sequence 28, Appl
39	161.5	30.8	768	8	US-08-806-029-35	Sequence 35, Appl
40	161.5	30.8	884	14	US-10-117-931-15	Sequence 15, Appl
41	161.5	30.8	889	8	US-08-806-029-19	Sequence 19, Appl
42	161.5	30.8	983	16	US-10-845-936A-37	Sequence 37, Appl
43	161.5	30.8	1027	16	US-10-845-936A-32	Sequence 32, Appl
44	161.5	30.8	1105	16	US-10-845-936A-33	Sequence 33, Appl
45	161.5	30.8	1125	16	US-10-845-936A-34	Sequence 34, Appl

```

US-10-210-1172-40
RESULT 1
Sequence 40, Application US/102101172
Publication No. US20040043928A1
GENERAL INFORMATION:
APPLICANT: Applicant, Ramesh
APPLICANT: Miller, Charles
APPLICANT: Paturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Rieger, Daniel
APPLICANT: Shmets, Richard
APPLICANT: Zernusen, Bryan
APPLICANT: Li, Li
APPLICANT: Ji, Weizhen
APPLICANT: Padigaru, Muralidhara
APPLICANT: Casman, Steacie
APPLICANT: Voss, Edward
APPLICANT: Boldog, Ferenc
APPLICANT: Gorman, Linda
APPLICANT: Leite, Mario
APPLICANT: Verneic, Corine
APPLICANT: Anderson, David
APPLICANT: Guo, Xiaojia
APPLICANT: Zhong, Mei
APPLICANT: Gerlach, Valerie
APPLICANT: Hjalte, Torb
APPLICANT: Rasetelli, Luca
APPLICANT: Spytek, Kimberly
APPLICANT: Edinger, Shlomit
APPLICANT: Eilerman, Karen
APPLICANT: Malyanek, Uriel
APPLICANT: Macdougall, John
APPLICANT: Stone, David
APPLICANT: Altsbrock II, John

```

```
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-416 A
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/309,501
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/323,994
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/373,814
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/310,951
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,544
PRIOR FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311,979
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/313,201
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/312,892
PRIOR FILING DATE: 2001-08-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 327
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 40
LENGTH: 692
TYPE: PRT
ORGANISM: Homo sapiens
US-10-210-172-40
```

```
Query Match      98.3%; Score 515; DB 15; Length 692;
Best Local Similarity 100.0%; Pred. No. 1.9e-31;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIIPGVPGVPPGAGLGGALGPGGKPLKVPGLAGAGLGAAPPAVT 62
DB 27 GGVPGAIIPGVPGVPPGAGLGGALGPGGKPLKVPGLAGAGLGAAPPAVT 86
QY 63 PFGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100
DB 87 PFGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 124
```

```
RESULT 2
US-10-210-172-38
Sequence 38, Application US/10210172
Publication No. US20040043928A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Rameesh
APPLICANT: Miller, Charles
APPLICANT: Patuturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Rieger, Daniel
APPLICANT: Shimkets, Richard
APPLICANT: Zerhusen, Bryan
APPLICANT: Li, Li
APPLICANT: Uj, Weizhen
APPLICANT: Padigaru, Muralidhara
APPLICANT: Casman, Stacie
APPLICANT: Voss, Edward
APPLICANT: Boldog, Ferenc
APPLICANT: Gorman, Linda
APPLICANT: Leite, Mario
APPLICANT: Vermet, Corine
APPLICANT: Anderson, David
APPLICANT: Guo, Xiaojia
APPLICANT: Zhong, Wei
APPLICANT: Gerlach, Valerie
APPLICANT: Hjalte, Tord
```

```
APPLICANT: Rastelli, Luca
APPLICANT: Spytek, Kimberly
APPLICANT: Edinger, Shlomitz
APPLICANT: Ellerman, Karen
APPLICANT: Malpankar, Uriel
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Alsebrook II, John
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-416 A
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/309,501
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/323,994
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/373,814
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/310,951
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,544
PRIOR FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311,979
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/313,201
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/312,892
PRIOR FILING DATE: 2001-08-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 327
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 38
LENGTH: 711
TYPE: PRT
ORGANISM: Homo sapiens
US-10-210-172-38
```

```
Query Match      98.3%; Score 515; DB 15; Length 711;
Best Local Similarity 100.0%; Pred. No. 1.9e-31;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIIPGVPGVPPGAGLGGALGPGGKPLKVPGLAGAGLGAAPPAVT 62
DB 27 GGVPGAIIPGVPGVPPGAGLGGALGPGGKPLKVPGLAGAGLGAAPPAVT 86
QY 63 PFGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100
DB 87 PFGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 124
```

```
RESULT 3
US-09-961-403-8
Sequence 8, Application US/09961403
Publication No. US20030077589A1
GENERAL INFORMATION:
APPLICANT: HE-STUMP, HOLGER
APPLICANT: HAENDLER, BERNARD
APPLICANT: KRAETZSCHMAR, JOERN
APPLICANT: KREFT, BERTHOLT
APPLICANT: WINTERHAGER, ELKE
APPLICANT: REGIDOR, PEDRO
APPLICANT: SCOTTI, SIMONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
FILE REFERENCE: SCH-1789
CURRENT APPLICATION NUMBER: US/09/961,403
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
```

; LENGTH: 731

APPLICANT: ONLY, Isabelle

```
/ TITLE OF INVENTION: Stimulation of the activity of an isoform of lysyl oxidase
/ TITLE OF INVENTION: for combating against some pathologies due to an incomplete,
/ TITLE OF INVENTION: absent or disorganized elastogenesis
/ FILE REFERENCE: 11123.82US01
/ CURRENT APPLICATION NUMBER: US/10/852,575
/ PRIOR FILING DATE: 2004-05-24
/ PRIOR APPLICATION NUMBER: FR 03 07178
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 788
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-852-575-3

Query Match
Best Local Similarity 98.3%; Score 515; DB 16; Length 788;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPAIPGGVPGVFPAGAGLGGALGPGKPLKPVPGLAGAGLGAFFAVT 62
DB 27 GGVPAIPGGVPGVFPAGAGLGGALGPGKPLKPVPGLAGAGLGAFFAVT 86
QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100
DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 124

RESULT 8
US-10-104-047-2915
/ Sequence 2915, Application US/10104047
/ Publication No. US20030236392A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: NO. US20030236392A1 full length cDNA
/ FILE REFERENCE: H1-A0105
/ CURRENT APPLICATION NUMBER: US/10/104,047
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2915
/ LENGTH: 617
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-104-047-2915

Query Match
Best Local Similarity 85.5%; Score 448; DB 15; Length 617;
Matches 88; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 GGVPAIPGGVPGVFPAGAGLGGALGPGKPLKPVPGLAGAGLGAFFAVT 62
DB 27 GGVPAIPGGVPGVFPAGAGLGGALGPGKPLKPVPGLAGAGLGAFFAVT 76
QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100
DB 77 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 114

RESULT 9
US-10-108-260A-2477
/ Sequence 2477, Application US/10108260A
/ Publication No. US20040005560A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: NO. US20040005560A1 full length cDNA
/ FILE REFERENCE: H1-A0106
/ CURRENT APPLICATION NUMBER: US/10/108,260A
/ PRIOR FILING DATE: 2002-03-27
/ NUMBER OF SEQ ID NOS: 5458
```

```
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2477
/ LENGTH: 663
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-108-260A-2477

Query Match
Best Local Similarity 63.8%; Score 334.5; DB 15; Length 663;
Matches 67; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

QY 3 GGVPAIPGGVPGVFPAGAGLGGALGPGKPLKPVPGLAGAGLGAFFAVT 62
DB 27 GGVPAIPGGVPGVFPAGAGLGGALGPGKPLKPVPGLAGAGLGAFFAVT 76
QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 100
DB 77 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVS 93

RESULT 10
US-08-806-029-27
/ Sequence 27, Application US/08806029
/ Publication No. US20020045567A1
/ GENERAL INFORMATION:
/ APPLICANT: Cappello, Joseph
/ APPLICANT: Stedronsky, Erwin R.
/ TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
/ TITLE OF INVENTION: Delivery and Tissue Augmentation
/ NUMBER OF SEQUENCES: 36
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
/ STREET: Four Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/806,029
/ FILING DATE: 24-FEB-1997
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/212,237
/ FILING DATE: 11-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Trecartin, Richard F.
/ REGISTRATION NUMBER: 31,801
/ REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 832 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
US-08-806-029-27

Query Match
Best Local Similarity 33.2%; Score 174; DB 8; Length 832;
Matches 53; Conservative 6; Mismatches 32; Indels 44; Gaps 7;

QY 4 GVPG-AIPG-GVPG-----GVFPAGAGLGLGGALGPGKPLKPVPGLAGAGLGA 57
DB 10 GVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 64
```



```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/806,029
FILING DATE: 24-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,237
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Treacartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58847-2/RPT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 936 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-806-029-26

Query Match      33.0%; Score 173; DB 8; Length 936;
Basic Local Similarity 34.8%; Pred. No. 3e-05; 35; Indels 62; Gaps 7
Matches 55; Conservative 6; Mismatches 35; Indels 62; Gaps 7

QY      4  GVPG-AIPG-GVPG-----GVFPYPGAGLGGALGGALVPG----- 35
      |||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db      10  GVPGGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGV 69
      |||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||

QY      36  -----GPELRVPG-GIAGAGLGGAGLAFPAVTPPGALVPG----- 70
      |||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db      129 -----GPELRVPG-GIAGAGLGGAGLAFPAVTPPGALVPG----- 129
      |||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||

```

OY 71 -----GVADAAAAYKAKAGAGGGVPGVG--GLGV 99
 || | : || | || | || : ||
Db 130 VPGWGPFGVGPVGAGAGSGGAGAGVSPGVGPVG 167

RESULT 15
US-10-117-931-25
; Sequence 25, Application US/10117931
; Publication No. US20030104589A1
; GENERAL INFORMATION:
; APPLICANT: STEDRONSKY, Erwin R.
; CAPELLO, Joseph
; TITLE OF INVENTION: Tissue Adhesive Using Synthetic
; Crosslinking
; METHOD OF ATTACHMENT:

ADDRESSSE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
 STREET: Four Embarcadero Center, Suite 200
 CITY: San Francisco
 STATE: CA
 COUNTRY: US
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/1117, 931
 FILING DATE: 05-Apr-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/642,246
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: ROWLAND, Berttram I
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: A61127-1/BI R

THIS PAGE IS BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2005, 07:25:52 ; Search time 24.3781 Seconds
(Without alignments)
394.685 Million cell updates/sec

Title: US-09-743-818a-4_COPY_1_100

Perfect score: 524

Sequence: 1 SMGVPGALPGVPGVFP.....AAKAGGLGVPVGLGVS 100

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	515	98.3	792	1 EAHU	elastin precursor,
2	377	71.9	860	1 EAMS	elastin precursor
3	326.5	62.3	864	1 EART	elastin precursor
4	326	62.2	770	2 S59623	tropoelastin - she
5	324.5	61.9	747	1 EABO	elastin precursor,
6	310	59.2	784	2 A26601	elastin precursor
7	148	28.2	158	2 T08957	glycine-rich prote
8	148	28.2	733	2 T05389	probable serine-th
9	146.5	28.0	212	2 E86179	hypothetical prote
10	144.5	27.6	641	1 Q08B31	nuclear antigen EB
11	141	26.9	376	2 T10455	heat shock related
12	136.5	26.0	767	2 E70895	hypothetical glyci
13	136	26.0	447	2 G84687	probable disease r
14	136	26.0	1489	2 D70807	hypothetical glyci
15	136	26.0	1901	2 T05442	hypothetical glyci
16	135	25.8	608	2 F70806	glycine-rich prote
17	134.5	25.7	907	2 A45560	sporozoite surface
18	133.5	25.5	882	2 B70812	hypothetical glyci
19	132.5	25.3	162	2 S56703	glycine-rich cell
20	131	25.0	338	1 KNMU	glycine-rich cell
21	131	25.0	384	1 A26099	glycine-rich cell
22	130.5	24.9	718	2 A36068	major amputate fi
23	129.5	24.7	543	2 F70726	hypothetical glyci
24	128.5	24.5	132	2 S14977	glycine-rich prote
25	127.5	24.3	87	2 T14302	glycine-rich cell
26	127.5	24.3	2038	2 A43742	female sterile hom
27	127	24.2	210	2 J01060	glycine-rich prote
28	127	24.2	783	2 E70824	hypothetical glyci
29	125.5	24.0	925	2 JC2033	G protein-coupled

30	125	23.9	1147	1 MMAXIB	myosin heavy chain
31	124.5	23.8	307	2 T27609	hypothetical prote
32	124.5	23.8	749	2 A70812	hypothetical glyci
33	124	23.7	228	2 T49891	glycine-rich prote
34	124	23.7	515	2 H70663	hypothetical glyci
35	124	23.7	778	2 F70963	hypothetical glyci
36	124	23.7	1660	2 A70869	hypothetical prote
37	123.5	23.6	479	2 F70573	hypothetical glyci
38	123.5	23.6	512	2 S70644	annexin VII - Afri
39	123	23.5	201	2 T00799	hypothetical prote
40	123	23.5	256	2 A70514	hypothetical glyci
41	122.5	23.4	271	2 S34666	glycine-rich prote
42	122.5	23.4	603	2 A70770	hypothetical glyci
43	121.5	23.2	112	2 J01063	glycine-rich prote
44	121.5	23.2	173	2 J01064	glycine-rich prote
45	121.5	23.2	220	2 T14441	glycine-rich prote

ALIGNMENTS

RESULT 1

EAHU elastin precursor, long splice form - human

N;Alternate names: tropoelastin

C;Species: Homo sapiens (man)

C;Date: 22-Jun-1990 #sequence, revision 26-Jul-1996 #text_change 09-Jul-2004

C;Accession: A32707, A33705, A30524, A53891

R;Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenblom, J

Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987

A;Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of c

A;Reference number: A32707, PMID:87289668; PMID:3039501

A;Accession: A32707

A;Molecule type: mRNA

A;Residues: 1-500,507-792 <IND>

A;Cross-references: UNIPROT:P15502; UNIPROT:Q9UMK5; GB:M16983; GB:J02948

J. Biol. Chem. 264, 8887-8891, 1989

A;Title: Characterization of the complete human elastin gene. Delineation of unusual fe

A;Reference number: A33705; PMID:8925358; PMID:2722804

A;Accession: A33705

A;Molecule type: DNA

A;Residues: 1-27 <BAS>

A;Cross-references: GB:J04821; NID:G182052; PIDN:AA52379.1; PID:G553276

R;Fezio, M.J.; Olsen, D.R.; Kaun, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N

J. Invest. Dermatol. 91, 458-464, 1988

A;Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant

A;Reference number: A30524; PMID:8900960; PMID:3171221

A;Accession: A30524

A;Molecule type: mRNA

A;Residues: 1-453,483-617,651-792 <FAZ>

A;Cross-references: EMBL:M56860; NID:G182061; PIDN:AA52382.1; PID:G182062

A;Note: This sequence represents a composite of several splice forms

R;Fezio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenblom, J.;

Lab. Invest. 58, 270-277, 1988

A;Title: Isolation and characterization of human elastin cDNAs, and age-associated vari

A;Reference number: A53891; PMID:8156138; PMID:2831431

A;Accession: A53891

A;Molecule type: mRNA

A;Residues: 164-453,483-500,507-617,651-792 <FA2>

A;Cross-references: GB:M24782; NID:G182063; PIDN:AA53190.1; PID:G182064

C;Comment: The term tropoelastin refers to a soluble precursor form of the extracellular

line oxidase activity.

C;Genetics:

A;Gene: GDB:ELN

A;Cross-references: GDB:119107; OMIM:130160

A;Map position: 7q11.23-7q11.23

C;Superfamily: elastin

C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine

F;1-26/Domain: signal sequence #status predicted <SIG>

F;27-792/Product: elastin #status predicted <MNT>

F;782-787/Disulfide bonds: #status predicted

Query Match 98.3%; Score 515; DB 1; Length 792;
 Best Local Similarity 100.0%; Pred. No. 1.4e-30;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGVPGAIPEGVPGVYFPAGLGGALGPGKPLKVPGLAGAGLGAFAFPVNT 62
 |||||
 Db 27 GGVPGAIPEGVPGVYFPAGLGGALGPGKPLKVPGLAGAGLGAFAFPVNT 86
 |||||
 Qy 63 FPGALVPGGVADAAAAYKAKAGAGLGGVPGVGGVGS 100
 |||||
 Db 87 FPGALVPGGVADAAAAYKAKAGAGLGGVPGVGGVGS 124
 |||||

RESULT 2

EAMS

elastin precursor - mouse
 N/Alternate names: tropoelastin
 C/Species: Mus musculus (house mouse)
 C/Date: 18-Aug-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
 C/Accession: A55721

R.Wyther, K.S.; Sechler, J.L.; Boyd, C.D.; Passmore, H.C.
 Genomics 23, 125-131, 1994
 A/Title: Use of an intron length polymorphism to localize the tropoelastin gene to mouse
 F/1-21/Domains: signal sequence #status predicted <StG>
 F/28-860/Product: elastin #status predicted <MAT>
 F/850-855/Disulfide bonds: #status predicted

A/Reference number: A55721; MUID:95130069; PMID:7829060
 A/Accession: A55721
 A/Molecule type: mRNA
 A/Residues: 1-860 <MYD>

A/Cross-references: UNIPROT:P54320; GB:U08210; NID:g473273; PIDN:AAA80155.1; PID:g473274
 A/Status: translated from GB/EMBL/DBJ
 C/Genetics:
 A/Map position: 5

C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine
 F/1-21/Domains: signal sequence #status predicted <StG>
 F/28-860/Product: elastin #status predicted <MAT>
 F/850-855/Disulfide bonds: #status predicted

Query Match 71.9%; Score 377; DB 1; Length 860;
 Best Local Similarity 72.6%; Pred. No. 1.7e-20;
 Matches 82; Conservative 4; Mismatches 11; Indels 16; Gaps 5;

Qy 3 GGVPGAIPEGVPGVYFPAGLGGALGPGKPLK-----VPGLAGAG 50
 |||||
 Db 32 GAVPGGLPGGVPGVYFPAGLGGALGPGKPLKPGAGLGTFGAGPGGAGAG 91
 |||||
 Qy 51 LGAGGAFPAVTFP--GALVPGGVADAAAAYK-AAKAGAGLGGVPGV-GGLGV 99
 |||||
 Db 92 PGAGLGAFFPAITFPAGALVPGAGAAAAYKAAKAGAGLGGVPGVGV 144
 |||||

RESULT 3

EART

elastin precursor - rat
 N/Alternate names: tropoelastin
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 11-Jan-1991 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
 C/Accession: A36106; A30878; A36523; S02173; I54172; I68505

R.Pierce, R.A.; Deak, S.B.; Stolle, C.A.; Boyd, C.D.
 Biochemistry 29, 9677-9683, 1990
 A/Title: Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.
 A/Reference number: A36106; MUID:91104868; PMID:1702999
 A/Accession: A36106

A/Cross-references: UNIPROT:Q99372; GB:M60647; GB:J05292; NID:g207444; PIDN:AAA42269.1;
 R/Deak, S.B.; Pierce, R.A.; Belisky, S.A.; Riley, D.J.; Boyd, C.D.
 J. Biol. Chem. 263, 13504-13507, 1988
 A/Title: Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.
 A/Reference number: A30878; MUID:88330866; PMID:2971041

A/Accession: A30878
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 781-864 <DEA>

A/Cross-references: GB:J04035; NID:g207442; PIDN:AAA42268.1; PID:g207443

R.Franzblau, C.; Prate, C.A.; Faris, B.; Colaninno, N.M.; Offner, G.D.; Mogyaszal Jr., P.
 J. Biol. Chem. 264, 15115-15119, 1989
 A/Title: Role of tropoelastin fragmentation in elastogenesis in rat smooth muscle cells.
 A/Reference number: A36523; MUID:89359227; PMID:2768256

A/Accession: A36523
 A/Molecule type: protein
 A/Residues: 22-31 <FRA>
 R/Rich, C.B.; Foster, J.A.
 Arch. Biochem. Biophys. 268, 551-558, 1989

A/Title: Characterization of rat heart tropoelastin.
 A/Reference number: S02173; MUID:89117149; PMID:2913947
 A/Accession: S02173

A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 19, 369-545, 548-764, 770-864 <RIC>

A/Experimental source: heart
 R/Pierce, R.A.; Alatawi, A.; Deak, S.B.; Boyd, C.D.
 Genomics 12, 651-658, 1992

A/Title: Elements of the rat tropoelastin gene associated with alternative splicing.
 A/Reference number: I54172; MUID:92241859; PMID:1572637
 A/Accession: I54172

A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 264-533 <RES>
 A/Cross-references: GB:M86372; NID:g207455; PIDN:AAA42271.1; PID:g554527

A/Accession: I68505
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 558-864 <RE2>

A/Cross-references: GB:M86376; NID:g207459; PIDN:AAA42272.1; PID:g207462
 C/Genetics:
 A/Intons: 277/1; 292/1; 308/1; 339/1; 359/1; 419/1; 437/1; 467/1; 484/1; 601/1; 621/1;
 A/Note: the list of introns may be incomplete

C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine
 F/1-21/Domains: signal sequence #status predicted <StG>
 F/22-864/Product: elastin #status predicted <MAT>
 F/854-859/Disulfide bonds: #status predicted

Query Match 62.3%; Score 326.5; DB 1; Length 864;
 Best Local Similarity 67.3%; Pred. No. 8.1e-17;
 Matches 74; Conservative 5; Mismatches 16; Indels 15; Gaps 5;

Qy 3 GGVPGAIPEGVPGVYFPAGLGGALGPGKPLK-----VPGLAGAGL 51
 |||||
 Db 30 GGVPGGLPGGVPGVYFPAGLGGALGPGKPLKPGAGLGTFGAGPGGAGAG 89
 |||||
 Qy 52 GAGLGAFFPAVTFPAGALVPGGVADAAAAYK-AAKAGAGLGGVPGV-GGLGV 99
 |||||
 Db 90 GAGLSY--ASRPGVLVPGGAGAAAAYKAAKAGAGLGGVPGVGV 137
 |||||

RESULT 4

S59623

tropoelastin - sheep
 C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C/Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S59623; A24758

R/Mauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.; BC
 Matrix Biol. 14, 635-641, 1994
 A/Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene.
 A/Reference number: S59623

A/Accession: S59623
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA

A/Residues: 1-770 <MAU>
 A/Cross-references: UNIPROT:P11547
 R/Tyoom, K.; Davidson, J.M.; Boyd, C.; May, M.; LaValle, P.; Ornstein-Goldstein, N.; Smir
 Arch. Biochem. Biophys. 241, 684-691, 1985

A/Title: Analysis of the 3' region of the sheep elastin gene.
 A/Reference number: A24758; MUID:85305763; PMID:3839997
 A/Accession: A24758
 A/Molecule type: mRNA

A:Residues: 655-669, 671-716, 732-770 <YOO>
C:Superfamily: elastin
C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F:760-765/Disulfide bonds: #status predicted

Query Match 62.2%; Score 326; DB 2; Length 770;
Best Local Similarity 67.9%; Pred. No. 8, 1e-17;
Matches 72; Conservative 4; Mismatches 22; Indels 8; Gaps 4;

QY 3 GGVPGAIPGGVPGGVFPFGAGLGGALGPGGKPLKVPVGGLAGAGLGA-GLGAPPAV 61
27 GGVTGAVPGGVPGGVFPFGAGLGGALGPGGKPLKVPVGGLAGAGLGAESGGLPAG 86

Db 62 TFFGAL--VPGGVADAAAAYK-AAKAGA---GLGVPVGGVGLGVS 100
87 AFPGFPGAGGGAAGAAAYKAAKAGAGLGGVGGVGGVGLGVS 132

RESULT 5
elastin precursor, splice form a - bovine
N:Alternate names: tropoelastin
N:Containing: elastin precursor, splice form b; elastin precursor, splice form c
C:Species: Bos primigenius taurus (cattle)
C>Date: 08-Jun-1989 #sequence revision 26-Jul-1996 #text change 09-Jul-2004
C:Accession: AJ1865; A26728; B26728; C26728; A22343; I45886
R:Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abrams, Biochemistry 28, 2365-2370, 1989
A>Title: Structure of the bovine elastin gene and S1 nuclease analysis of alternative splicing
A:Reference number: AJ1865; MUID:89274159; PMID:253440
A:Accession: A31865
A:Molecule type: DNA
A:Residues: 1-27 <YEH>
A:Cross-references: UNIPROT:P04985; UNIPROT:Q28101; GB:J02855; NID:G340504; PID:AAA3077
R:Raju, K.; Anwar, R.A.
J. Biol. Chem. 262, 5755-5762, 1987
A>Title: Primary structures of bovine elastin a, b, and c deduced from the sequences of complementary DNAs
A:Reference number: A92640; MUID:87194772; PMID:3032943
A:Accession: A26728
A:Molecule type: mRNA
A:Residues: 1, 'RS', '4-11', 'E', '13-636', 'V', '638-747' <RAU>
A:Cross-references: GB:J02717; NID:g163019; PID:AAA30503.1; PID:g163020
A:Accession: B26728
A:Molecule type: mRNA
A:Residues: 1, 'RS', '4-11', 'E', '13-225', '240-636', 'V', '638-747' <RA2>
A:Cross-references: GB:K03505; NID:g163025; PID:AAA30505.1; PID:g163026
A:Accession: C26728
A:Molecule type: mRNA
A:Residues: 1, 'RS', '4-11', 'E', '13-225', '260-636', 'V', '638-747' <RA3>
A:Cross-references: GB:K03506; NID:g163027; PID:AAA30506.1; PID:g163028
R:Gicla, G.; May, M.; Ornstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rosenblum, Biochemistry 24, 3075-3080, 1985
A>Title: Structure of the 3' portion of the bovine elastin gene.
A:Reference number: A22343; MUID:85280426; PMID:2992576
A:Accession: A22343
A:Molecule type: DNA
A:Residues: 613-747 <CIC>
A:Cross-references: GB:M20415
R:Rosenbloom, J.
Lab. Invest. 51, 605-623, 1984
A>Title: Biology of disease: Elastin: Relation of protein and gene structure to disease.
A:Reference number: I45885; MUID:85059254; PMID:6150137
A:Accession: I45886
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 678-683, 685-747 <ROS>
A:Cross-references: GB:M31988; NID:g163015; PID:AAA96417.1; PID:g163018
R:Brown, P.L.; Mecham, U.; Tiedale, C.; Mecham, R.P.
Biochem. Biophys. Res. Commun. 186, 549-555, 1992
A>Title: The cysteine residues in the carboxy terminal domain of tropoelastin form an intramolecular disulfide bond
A:Reference number: A56621; MUID:92337651; PMID:1632791
A:Contents: annotation, disulfide bonds
C:Comment: The term tropoelastin refers to a soluble precursor form of the extracellular

ine oxidase activity.
C:Genetics:
A:Introns: 634/3; 653/3; 676/3; 689/3; 707/3; 716/3; 733/3
A>Note: the list of introns is incomplete
C:Superfamily: elastin
C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F:1-747/Product: elastin precursor, splice form a #status predicted <EPA>
F:1-225, 260-747/Product: elastin precursor, splice form c #status predicted <EPC>
F:1-225, 240-747/Product: elastin precursor, splice form b #status predicted <EPB>
F:1-26/Domain: signal sequence #status predicted <SIS>
F:27-747/Product: elastin #status predicted <MNT>
F:105, 109, 252, 271, 275, 324, 327, 400, 404, 407, 445, 448, 489, 493, 544, 548, 552, 606, 609, 645, 649, 673, 737-742/Disulfide bonds: #status experimental

Query Match 61.9%; Score 324.5; DB 1; Length 747;
Best Local Similarity 68.3%; Pred. No. 1e-16;
Matches 71; Conservative 4; Mismatches 22; Indels 7; Gaps 4;

QY 3 GGVPGAIPGGVPGGVFPFGAGLGGALGPGGKPLKVPVGGLAGAGLGAAPPVAV 62
27 GGVTGAVPGGVPGGVFPFGAGLGGALGPGGKPLKVPVGGLAGAGLGAESGALP-A 85

Db 63 FFGAL--VPGGVADAAAAYK-AAKAGA---GLGVPVGGVGLGVS 100
86 FPGGFPGAGGGAAGAAAYKAAKAGAGLGGVGGVGGVGLGVS 129

RESULT 6
elastin precursor - chicken (fragment)
N:Alternate names: tropoelastin
C:Species: Gallus gallus (chicken)
C>Date: 05-Oct-1988 #sequence revision 26-Jul-1996 #text change 09-Jul-2004
C:Accession: A26601; A30795; A27264
R:Bressan, G.M.; Argos, P.; Stanley, K.K.
Biochemistry 26, 1497-1503, 1987
A>Title: Repeating structure of chick tropoelastin revealed by complementary DNA cloning
A:Reference number: A26601; MUID:87242320; PMID:3539675
A:Accession: A26601
A:Molecule type: mRNA
A:Residues: 1-212, 237-524, 535-784 <BR2>
A:Cross-references: UNIPROT:P07916; GB:M15889; NID:g212803; PID:AAA49108.1; PID:g21280
R:Baule, V.J.; Foster, J.A.
Biochem. Biophys. Res. Commun. 154, 1054-1060, 1988
A>Title: Multiple chick tropoelastin mRNAs.
A:Reference number: A30795; MUID:88309083; PMID:2841924
A:Accession: A30795
A:Molecule type: mRNA
A:Residues: 85-784 <BAU>
A:Cross-references: GB:M21880; NID:g212741; PID:AAA49082.1; PID:g212742
R:Tokimatsu, I.; Tajima, S.; Nishikawa, T.; Tajima, M.; Fukasawa, T.
Arch. Biochem. Biophys. 256, 455-461, 1987
A>Title: Sequence analysis of elastin cDNA from chick aorta and tissue-specific transcripts
A:Reference number: A27264; MUID:87297534; PMID:3502711
A:Accession: A27264
A:Molecule type: mRNA
A:Residues: 491-569, 'G', '571-604', 'A', '606-643', 'A', '645-687', 'R', '689-700', 'R', '702-784' <TOX>
A:Cross-references: GB:M18633; NID:g211742; PID:AAA48761.1; PID:g211743
C:Superfamily: elastin
C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F:1-24/Domain: signal sequence (fragment) #status predicted <SIG>
F:25-212, 237-524, 535-784/Product: elastin #status predicted <MNT>
F:773-779/Disulfide bonds: #status predicted

Query Match 59.2%; Score 310; DB 2; Length 784;
Best Local Similarity 61.6%; Pred. No. 1.2e-15;
Matches 69; Conservative 3; Mismatches 18; Indels 22; Gaps 4;

QY 3 GGVPGAIP-GGVPGVFPFGAGLGGALGPGGKPLKVPVGGLAG----- 48
25 GGVTGAVPGGVPGGVFPFGAGLGGALGPGGKPLKVPVGGLAGLGPAGCA 84

Db 49 --AGLGGAGLGAAPPVAVFPFGALVPGGVADAAAAYKAAKAGLGGVGGVGLG 98

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C/Accession: F70806
 R/Cole, S.T.; Brosch, R.; Parhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A/Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A/Reference number: A70500; MUID:98295987; PMID:9634230
 A/Accession: F70806
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-1901 <COL>
 A/Cross-references: UNIPROT:O53553; GB:AL022022; GB:AL123456; NID:93261554; PIDN:CAA1774
 A/Experimental source: strain H37Rv
 C/Genetics:
 A/Gene: RV3508
 C/Superfamily: collagen alpha 1(IV) chain

Query Match 26.0%; Score 136; DB 2; Length 1901;
 Best Local Similarity 37.7%; Pred. No. 0.012;
 Matches 43; Conservative 3; Mismatches 50; Indels 18; Gaps 4;
 QY 3 GGVPGAIPG---GVPGVFPYFGAGLGGALGPG---KPLKVPQGLAGAGLGG 54
 |||||
 Db 192 GGVGAGGGGTGAGGPGGLIWGGGAGGVGAGGTCGAGRAELLFGAGGAGAGTDDG 251
 QY 55 LGAFPAVTPPGA-----LVPGGVADA--AAATQAAKAGAGLGGVPGVGGIG 98
 |||||
 Db 252 PGATGTTGGHGGVGGDGGWLAPGAGAGGAGGAGGAGSDGALGGTGTGTG 305

Search completed: August 10, 2005, 07:38:34
 Job time : 25.3781 secs

THIS PAGE IS BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2005, 07:17:42 ; Search time 111.94 Seconds

(without alignments)
457.457 Million cell updates/sec

Title: US-09-743-818a-4_COPY_1_100

Sequence: 1 SMGVPGALPGVPGVPGVFP.....AAKAGAGLGVPVGLGVS 100

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	515	98.3	658	06P014	06P014 homo sapien
2	515	98.3	687	014235	014235 homo sapien
3	515	98.3	711	0723F5	0723F5 homo sapien
4	515	98.3	730	EL5_HUMAN	EL5502 homo sapien
5	515	98.3	757	014234	014234 homo sapien
6	515	98.3	757	075MUS	075MUS homo sapien
7	503	96.0	602	015337	015337 homo sapien
8	503	96.0	635	015336	015336 homo sapien
9	448	85.5	559	06ZUN2	06ZUN2 homo sapien
10	448	85.5	687	072316	072316 homo sapien
11	438	83.6	643	08NB14	08NB14 homo sapien
12	377	71.9	860	EL5_MOUSE	EL5330 mus musculu
13	377	71.9	860	08C9L8	08C9L8 mus musculu
14	375.5	71.7	472	08N2G0	08N2G0 homo sapien
15	351	67.0	570	06ZMW6	06ZMW6 homo sapien
16	326.5	62.3	864	EL5_RAT	EL5312 ratius norv
17	324.5	61.9	747	EL5_BOVIN	EL54985 bos taurus
18	313	59.7	750	09BD20	09BD20 macaca mula
19	310	59.2	750	EL5_CHICK	EL57916 gallus gall
20	283	54.0	810	09ES29	09ES29 mus musculu
21	245.5	46.9	650	028099	028099 bos taurus
22	245.5	46.9	666	028096	028096 bos taurus
23	245.5	46.9	679	028097	028097 bos taurus
24	245.5	46.9	707	028098	028098 bos taurus
25	171.5	32.7	258	09UMF5	09UMF5 homo sapien
26	166.5	31.8	524	081701	081701 araneus ven
27	166	30.2	1884	09NHM2	09NHM2 nephila ina
28	158.5	30.2	626	09NHM1	09NHM1 nephila ina
29	158.5	30.2	871	044358	044358 nephila cla
30	158.5	30.2	2249	09NHM4	09NHM4 nephila cla
31	157.5	30.1	717	06M166	06M166 bdellovibri

32	156	29.8	1002	2	Q9BIU8	Q9BIU8 argiope tri
33	155.5	29.7	907	2	044359	044359 nephila cla
34	155	29.6	563	2	06J6N0	06J6N0 araneus ven
35	154.5	29.5	651	2	09BIU9	09BIU9 argiope tri
36	152.5	29.1	441	2	093YR3	093YR3 aradidopsis
37	151.5	28.9	905	2	08MW55	08MW55 mytilus gal
38	148	28.2	158	2	Q9SA11	Q9SA11 streptomyce
39	148	28.2	783	2	Q9XA11	Q9XA11 aradidopsis
40	146.5	28.0	212	2	023018	023018 oceanobacil
41	145.5	27.8	246	2	08ES24	08ES24 oceanobacil
42	144.5	27.6	641	1	EBN1_EBV	P03211 Epstein-bar
43	144.5	27.6	641	2	Q777EI	Q777EI human herpe
44	144	27.5	279	2	Q6C3I2	Q6C3I2 yarrowia li
45	143.5	27.4	922	2	08MW53	08MW53 mytilus gal

ALIGNMENTS

RESULT 1
ID 06P014 PRELIMINARY; PRT; 658 AA.
AC 06P014;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE EBN protein.
GN Name=ELN;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tohiyuki S., Carninci P., Mullany S.J.,
RA Baha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyanski M.I., Skalska U., Smalusz D.E., Schmech A., Schein J.B.,
RT Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC65566; AA65566.1; -;
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR003979; Tropoelastin.
DR PROSITE; PS00101; HEXAPEP_TRANSPEPTASES; UNKNOWN 1.
SQ
SEQUENCE 658 AA; 56880 MW; 5DARC00D16A2F94E CRCK4;
Query Match 98.3%; Score 515; DB 2; Length 658;
Best local Similarity 100.0%; Pred. No. 5.4e-25;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 3 GGVPGAIIPGGVPGVFPYPPAGLGGALGPGKPLKVPVPGLAGAGLGAFFPVT 62
    |||
DB 27 GGVPGAIIPGGVPGVFPYPPAGLGGALGPGKPLKVPVPGLAGAGLGAFFPVT 86
QY 63 FPGALVPGGVADAAAAYKAKAGAGLGGVPGVGLGVS 100
    |||
DB 87 FPGALVPGGVADAAAAYKAKAGAGLGGVPGVGLGVS 124

RESULT 2
ID 014235 PRELIMINARY; PRT; 687 AA.
AC 014235;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Elastin.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.,
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA."
RT Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87274906; PubMed=3038460;
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA Rosenbloom J., Ornstein-Goldstein N.,
RT "Structure of the 3' region of the human elastin gene: great abundance
RT of Alu repetitive sequences and few coding sequences."
RT Connect. Tissue Res. 16:197-211(1987).
RN [3]
DB EMBL, M17282; AAC98393.1; -.
DB EMBL, M16983; AAC98393.1; JOINED.
DB EMBL, M17265; AAC98393.1; JOINED.
DB EMBL, M17266; AAC98393.1; JOINED.
DB EMBL, M17267; AAC98393.1; JOINED.
DB EMBL, M17268; AAC98393.1; JOINED.
DB EMBL, M17271; AAC98393.1; JOINED.
DB EMBL, M17272; AAC98393.1; JOINED.
DB EMBL, M17273; AAC98393.1; JOINED.
DB EMBL, M17275; AAC98393.1; JOINED.
DB EMBL, M17276; AAC98393.1; JOINED.
DB EMBL, M17277; AAC98393.1; JOINED.
DB EMBL, M17278; AAC98393.1; JOINED.
DB EMBL, M17279; AAC98393.1; JOINED.
DB EMBL, M17281; AAC98393.1; JOINED.
DB HSSP; P50099; 1ZFU.
DB GO; GO:0005578; Extracellular matrix (sensu Metazoa); NAS.
DB GO; GO:0030023; Extracellular matrix constituent conferring. . .; NAS.
DB InterPro; IPR001451; Hexapep_transf.
DB PRINTS; PR01500; TROPOLASTIN.
DB PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SQ SEQUENCE 687 AA; 59529 MW; 864068C4C8E9F88F CRC64;
```

```
DB 87 FPGALVPGGVADAAAAYKAKAGAGLGGVPGVGLGVS 124

RESULT 3
ID 0723F5 PRELIMINARY; PRT; 711 AA.
AC 0723F5;
DT 01-OCT-2003 (TRENBLREL. 25, Created)
DT 01-OCT-2003 (TRENBLREL. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Hypothetical protein DKFZp686F06102.
GN Name=DKFZp686F06102;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human fetal kidney;
RA Poustka A., Albert R., Moosmayer P., Schnupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amdt C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX537939; CDD97910.1; -.
DR InterPro; IPR001451; Hexapep_transf.
DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 711 AA; 61765 MW; 95B624A9B4A989B CRC64;

Query Match 98.3%; Score 515; DB 2; Length 711;
Best Local Similarity 100.0%; Pred. No. 5.8e-25;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGVPGAIIPGGVPGVFPYPPAGLGGALGPGKPLKVPVPGLAGAGLGAFFPVT 62
    |||
DB 27 GGVPGAIIPGGVPGVFPYPPAGLGGALGPGKPLKVPVPGLAGAGLGAFFPVT 86
QY 63 FPGALVPGGVADAAAAYKAKAGAGLGGVPGVGLGVS 100
    |||
DB 87 FPGALVPGGVADAAAAYKAKAGAGLGGVPGVGLGVS 124

RESULT 4
ELS HUMAN
ID 014235 STANDARD; PRT; 730 AA.
AC P15502; 014233; 014238;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Elastin precursor (Tropoelastin).
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.,
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA."
RT Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Skin fibroblast;
RX MEDLINE=89009960; PubMed=3171221;
RA Fazio M.J., Olsen D.R., Kaub E.A., Baldwin C.T., Indik Z.,
RA Ornstein-Goldstein N., Yeh H., Rosenbloom J., Uitto J.;
RL "Cloning of full-length elastin cDNAs from a human skin fibroblast
RL recombinant cDNA library: further elucidation of alternative splicing
RL utilizing exon-specific oligonucleotides."
RL J. Invest. Dermatol. 91:458-464(1988).
RN [3]
```

RP SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).

RC TISSUE=Placenta; PubMed=2831431;
 RA MEDLINE=88156138; PubMed=2831431;
 RA Fazio M.J., Olsen D.R., Kuivanen H., Chu M.L., Davidson J.M.,
 RA Rosenbloom J., Uitto J.;
 RA "Isolation and characterization of human elastin cDNAs, and age-
 RT associated variation in elastin gene expression in cultured skin
 RT fibroblasts.";
 RL Lab. Invest. 58:270-277(1988).
 RN [4]
 RN SEQUENCE OF 603-730 FROM N.A.
 RC TISSUE=Hippocampus, and Placenta;
 RA MEDLINE=96291399; PubMed=8699688; DOI=10.1016/S0092-8674(00)80077-X;
 RA Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J.,
 RA Robinson B.F., Klein B.F., Ewert G.J., Everett L.A., Green E.D.,
 RA Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,
 RA Keating M.T.;
 RA "Lim-kinase1 hemizyosity implicated in impaired visuospatial
 RT constructive cognition.";
 RT Cell 86:59-69(1996).
 RN [5]
 RN INVOLVEMENT IN CUTIS LAXA.
 RP MEDLINE=99091639; PubMed=9873040; DOI=10.1074/jbc.274.2.981;
 RA Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;
 RT "Cutis laxa arising from frameshift mutations in exon 30 of the
 RT elastin gene (ELN).";
 RL J. Biol. Chem. 274:981-986(1999).
 RN [6]
 RN INVOLVEMENT IN SVAS.
 RP PubMed=10942104;
 RA Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,
 RA Munnich A., Syskens B., Gewillig M., Devriendt K., Boyd C.D.;
 RA "Isolated supravalvular aortic stenosis: functional haploinsufficiency
 RT of the elastin gene as a result of nonsense-mediated decay.";
 RL Hum. Genet. 106:577-588(2000).
 CC -1- FUNCTION: Major structural protein of tissues such as aorta and
 CC nuchal ligament, which must expand rapidly and recover completely.
 CC -1- SUBUNIT: The polymeric elastin chains are cross-linked together
 CC into an extensible 3D network.
 CC -1- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC "IsoId=P15502-1; Sequence=Displayed;
 CC Name=2;
 CC "IsoId=P15502-2; Sequence=VSP_004243;
 CC -1- PTM: The crosslinks are made of deaminated lys.
 CC -1- DISEASE: Defects in ELN are a cause of autosomal dominant cutis
 CC laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder
 CC characterized by loose, hyperextensible skin with decreased
 CC resilience and elasticity leading to a premature aged appearance.
 CC The skin changes are often accompanied by extracutaneous
 CC manifestations, including pulmonary emphysema, bladder
 CC diverticula, pulmonary artery stenosis and pyloric stenosis.
 CC -1- DISEASE: Haploinsufficiency of ELN may be the cause of certain
 CC cardiovascular and musculo-skeletal abnormalities observed in
 CC Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare
 CC developmental disorder and a contiguous gene deletion syndrome
 CC involving genes from chromosome band 7q11.23.
 CC -1- DISEASE: Defects in ELN are the cause of supravalvular aortic
 CC stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of
 CC the ascending aorta which can occur sporadically, as an autosomal
 CC dominant condition, or as one component of Williams-Beuren
 CC syndrome.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).

CC EMBL; M17282; AAC98394.1; -;
 DR EMBL; M16983; AAC98394.1; JOINED.
 DR EMBL; M17265; AAC98394.1; JOINED.
 DR EMBL; M17266; AAC98394.1; JOINED.
 DR EMBL; M17267; AAC98394.1; JOINED.
 DR EMBL; M17268; AAC98394.1; JOINED.
 DR EMBL; M17270; AAC98394.1; JOINED.
 DR EMBL; M17271; AAC98394.1; JOINED.
 DR EMBL; M17272; AAC98394.1; JOINED.
 DR EMBL; M17273; AAC98394.1; JOINED.
 DR EMBL; M17275; AAC98394.1; JOINED.
 DR EMBL; M17276; AAC98394.1; JOINED.
 DR EMBL; M17277; AAC98394.1; JOINED.
 DR EMBL; M17278; AAC98394.1; JOINED.
 DR EMBL; M17279; AAC98394.1; JOINED.
 DR EMBL; M17280; AAC98394.1; JOINED.
 DR EMBL; M17281; AAC98394.1; JOINED.
 DR EMBL; M36860; AAA52382.1; -;
 DR EMBL; M24782; AAA53190.1; -;
 DR EMBL; U62292; AAB17544.1; -;
 DR EMBL; X15603; CAA33627.1; -;
 DR PIR; A32707; EAHU.
 DR HSSP; P50099; 1ZFU.
 DR Genew; HGNC:3327; ELN.
 DR MIM; 130160; -;
 DR MIM; 123700; -;
 DR MIM; 194050; -;
 DR MIM; 185500; -;
 DR GO; GO:0005578; C:extracellular matrix; TAS.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0008015; P:circulation; TAS.
 DR GO; GO:0009887; P:organogenesis; TAS.
 DR GO; GO:0007585; P:respiratory gaseous exchange; TAS.
 DR InterPro; IPRO03979; tropoelastin.
 DR PRINTS; PRO1500; TROPELASTIN.
 KW Alternative splicing; Repeat; Signal; Structural protein;
 KW Williams-Beuren syndrome.
 FT SIGNAL 1 26
 FT CHAIN 27 730 Elastin.
 FT DISUPID 720 725 By similarity.
 FT VARSPIC 472 477 Missing (in isoform 2).
 FT FTId=VSP_004243.
 SQ SEQUENCE 730 AA; 63260 MW; AB06D15BA567AE46 CRC64;
 Query Match 98.3%; Score 515; DB 1; Length 730;
 Best Local Similarity 100.0%; Pred. No. 5.9e-25;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GGVPGAIIPGVPGVFPAGAGLGGALGPGGKPLKPYVPGLAGAGLGAAPAVT 62
 Db 27 GGVPGAIIPGVPGVFPAGAGLGGALGPGGKPLKPYVPGLAGAGLGAAPAVT 86
 QY 63 FPGALVPGGVADAAAYKAKAKAGAGCGVGVGGLGV 100
 Db 87 FPGALVPGGVADAAAYKAKAKAGAGCGVGVGGLGV 124
 RESULT 5
 Q14234 PRELIMINARY; PRT; 757 AA.
 ID Q14234;
 AC Q14234;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DN Elastin.
 GN Name=ELN;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxId=9606;

```

RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=87289668; PubMed=3039501;
RA      Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA      Rosenbloom J.C., Peltonen L., Rosenbloom J.;
RT      "Alternative splicing of human elastin mRNA indicated by sequence
RT      analysis of cloned genomic and complementary DNA.";
RL      Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=87274906; PubMed=3038460;
RA      Indik Z., Yoon K., Morrow S.D., Cicilia G., Rosenbloom J.,
RA      Rosenbloom J., Ornstein-Goldstein N.;
RT      "Structure of the 3' region of the human elastin gene: great abundance
RT      of Alu repetitive sequences and few coding sequences.";
RL      Connect. Tissue Res. 16:197-211(1987).
DR      EMBL; M17282; AAC98395.1; -.
DR      EMBL; M16983; AAC98395.1; JOINED.
DR      EMBL; M17265; AAC98395.1; JOINED.
DR      EMBL; M17266; AAC98395.1; JOINED.
DR      EMBL; M17267; AAC98395.1; JOINED.
DR      EMBL; M17268; AAC98395.1; JOINED.
DR      EMBL; M17270; AAC98395.1; JOINED.
DR      EMBL; M17271; AAC98395.1; JOINED.
DR      EMBL; M17272; AAC98395.1; JOINED.
DR      EMBL; M17273; AAC98395.1; JOINED.
DR      EMBL; M17274; AAC98395.1; JOINED.
DR      EMBL; M17275; AAC98395.1; JOINED.
DR      EMBL; M17276; AAC98395.1; JOINED.
DR      EMBL; M17277; AAC98395.1; JOINED.
DR      EMBL; M17278; AAC98395.1; JOINED.
DR      EMBL; M17279; AAC98395.1; JOINED.
DR      EMBL; M17280; AAC98395.1; JOINED.
DR      EMBL; M17281; AAC98395.1; JOINED.
GO; GO:0005578; C:extracellular matrix (sensu Metazoa); NAS.
DR      GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.
DR      InterPro; IPR001451; Hexapep.transf.
DR      PRINTS; PR01500; TROPOELASTIN.
DR      PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ      SEQUENCE 757 AA; 66136 MW; 23B7F5B8AF85CA8 CRC64;

Query Match          98.3%; Score 515; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 6e-25;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GGVPGAI PGGVGVPYPPAGLGGALGGGALPGGKPLKVPVGLAGAGLGAAPPAYT 62
        |||||
DB      27 GGVPGAI PGGVGVPYPPAGLGGALGGGALPGGKPLKVPVGLAGAGLGAAPPAYT 86
        |||||

QY      63 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 100
        |||||
DB      87 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 124
        |||||

RESULT 6
ID      Q75MUS          PRELIMINARY;      PRT;      757 AA.
AC      Q75MUS;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Hypothetical protein ELN.
GN      Name=ELN;
OS      Homo sapiens (human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA      Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA      Wagner-McPherson C., Layman D., Maa J., Jaeger S., Walker R.,

```

```

RA      Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA      Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.B., Cordes M., Du H.,
RA      Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA      Vanhurn A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA      Ozerovsk P., Bellick L., Scott K., Holmes A., Harkins R., Harris A.,
RA      Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA      Kozlowski-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA      Tin-Lowell A.M., Abbott A., Mink P., Maupin R., Strommatt C.,
RA      Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA      Wendt M.C., Yang S.P., Schultz B.R., Wallis J.W., Spiech J.,
RA      Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,
RA      Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA      Clifton S.W., Chisose S.L., Marra M.A., Raymond C., Haugen E.,
RA      Gillett W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
RA      Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA      Baertsch R.A., Brent M.R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA      Bailey J.A., Portnoy M.E., Torrents D., Chitwalia A.T., Gish W.R.,
RA      Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA      Waterston R.H., Wilson R.K.;
RT      "The DNA sequence of human chromosome 7.";
RL      Nature 424:157-164(2003).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Waterston R.;
RL      Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Wilson R.;
RL      Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AC005056; AAS07435.1; -.
DR      GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR      GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR      InterPro; IPR001451; Hexapep.transf.
DR      InterPro; IPR003979; tropoelastin.
DR      PRINTS; PR01500; TROPOELASTIN.
DR      PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
KW      Hypothetical protein.
SQ      SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;

Query Match          98.3%; Score 515; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 6e-25;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GGVPGAI PGGVGVPYPPAGLGGALGGGALPGGKPLKVPVGLAGAGLGAAPPAYT 62
        |||||
DB      27 GGVPGAI PGGVGVPYPPAGLGGALGGGALPGGKPLKVPVGLAGAGLGAAPPAYT 86
        |||||

QY      63 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 100
        |||||
DB      87 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVS 124
        |||||

RESULT 7
ID      O15337          PRELIMINARY;      PRT;      602 AA.
AC      O15337;
DT      01-JAN-1998 (TrEMBLrel. 05, Created)
DT      01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Elastin (Fragment).
OS      Homo sapiens (human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97358574; PubMed=9215670; DOI=10.1093/hmg/6.7.1021;
RA      Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA      Morris C.A., Keating M.T.;
RT      "Elastin point mutations cause an obstructive vascular disease,
RT      supravalvular aortic stenosis.";
RL      Hum. Mol. Genet. 6:1021-1028(1997).
DR      EMBL; U93037; AAB65620.1; -.

```

DR EMBL: U93034; AAB65620.1; JOINED.
DR EMBL: U93035; AAB65620.1; JOINED.
DR EMBL: U93036; AAB65620.1; JOINED.
DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO: GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro: IPR001451; Hexapep.transf.
DR InterPro: IPR003979; tropoelastin.
DR PRINTS: PRO1500; TROPOELASTIN.
DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
FT NON TER 1
FT NON TER 602
SQ SEQUENCE 602 AA; 51807 MW; 53B5B9A71EF04807 CRC64;

Query Match 96.0%; Score 503; DB 2; Length 602;
Best Local Similarity 100.0%; Pred. No. 2.9e-24;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPGAIPGSGVPGVFPYPGAIGALGGALGPGKPLKVPVPGLAGAGLAGAFPAVTFP 64
DB 1 VPGAIPGSGVPGVFPYPGAIGALGGALGPGKPLKVPVPGLAGAGLAGAFPAVTFP 60

QY 65 GALVPGGVADAAAAYKAKAGAGLGGVPGVGLGVS 100
DB 61 GALVPGGVADAAAAYKAKAGAGLGGVPGVGLGVS 96

RESULT 8
015336 PRELIMINARY; PRT; 635 AA.

ID 015336;
AC 015336;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Elasin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97358574; PubMed=9215670; DOI=10.1093/hmg/6.7.1021;
RA I.D.Y., Toland A.B., Boak B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.
RT "Elastin point mutations cause an obstructive vascular disease,
RT supravulval aortic stenosis."
RL Hum. Mol. Genet. 6:1021-1028(1997).
DR EMBL: U93037; AAB65621.1; -.
DR EMBL: U93034; AAB65621.1; JOINED.
DR EMBL: U93035; AAB65621.1; JOINED.
DR EMBL: U93036; AAB65621.1; JOINED.
DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO: GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro: IPR001451; Hexapep.transf.
DR InterPro: IPR003979; tropoelastin.
DR PRINTS: PRO1500; TROPOELASTIN.
DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
FT NON TER 1
FT NON TER 635
SQ SEQUENCE 635 AA; 55279 MW; 72950C64127B2A4 CRC64;

Query Match 96.0%; Score 503; DB 2; Length 635;
Best Local Similarity 100.0%; Pred. No. 3e-24;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPGAIPGSGVPGVFPYPGAIGALGGALGPGKPLKVPVPGLAGAGLAGAFPAVTFP 64
DB 1 VPGAIPGSGVPGVFPYPGAIGALGGALGPGKPLKVPVPGLAGAGLAGAFPAVTFP 60

QY 65 GALVPGGVADAAAAYKAKAGAGLGGVPGVGLGVS 100
DB 61 GALVPGGVADAAAAYKAKAGAGLGGVPGVGLGVS 96

RESULT 9
06ZUN2 PRELIMINARY; PRT; 559 AA.
ID 06ZUN2;
AC 06ZUN2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ43523.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawano-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuna M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuno Y., Nagai K., Isogai T.,
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK125511; BAC86188.1; -.
DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO: GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro: IPR003979; tropoelastin.
DR PRINTS: PRO1500; TROPOELASTIN.
DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ SEQUENCE 559 AA; 53787 MW; 20938FEEC5492A01 CRC64;

Query Match 85.5%; Score 448; DB 2; Length 559;
Best Local Similarity 89.8%; Pred. No. 7.8e-21;
Matches 88; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 GGVPAIPGSGVPGVFPYPGAIGALGGALGPGKPLKVPVPGLAGAGLAGAFPAVTFP 62
DB 27 GGVPAIPGSGVPGVFPYPGAIGALGGALGPGKPLKVPVPGLAGAGLAGAFPAVTFP 76

QY 63 FGVALVPGGVADAAAAYKAKAGAGLGGVPGVGLGVS 100
DB 77 FGVALVPGGVADAAAAYKAKAGAGLGGVPGVGLGVS 114

RESULT 10
072316 PRELIMINARY; PRT; 687 AA.

ID 072316;
AC 072316;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZ686021208 (Fragment).
GN Name=DKFZ686021208;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Lauber J., Bahr A., Mewes H.W., Well B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX538199; CAD98065.1; -.
DR InterPro: IPR001451; Hexapep.transf.
DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
KM Hypothetical protein.
FT NON TER 1
FT NON TER 687
SQ SEQUENCE 687 AA; 59847 MW; 79232A191DC1F10F CRC64;

Query Match 85.5%; Score 448; DB 2; Length 687;
Best Local Similarity 89.8%; Pred. No. 9.1e-21;
Matches 88; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

```

Qy 3 GGVPGAIPEGVPGVFPYFGAGLGGALGPGKPLKPVGGLAGAGLGAFAFPAVT 62
    |||||
Db 37 GGVPGAIPEGVPGVFPYF-----ALGPGKRLKVPGGLAGAGLGAFAFPAVT 86
    |||||

Qy 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGGCGVS 100
    |||||
Db 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGGCGVS 124
    |||||

RESULT 11
Q8NB14 PRELIMINARY; PRT; 643 AA.
AC Q8NB14;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DS Hypothetical protein PSEC0254.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Makamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075554; BAC11696.1; -.
DR HSSP; P50099; 1ZFU.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005201; P:extracellular matrix structural constituent, IEA.
DR InterPro; IPR001451; Hexadep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROP0ELASTIN.
DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
DR SEQUENCE 643 AA; 55629 MW; PFC042617E72A69 CRC64;

Query Match
Best Local Similarity 83.6%; Score 438; DB 2; Length 643;
Matches 86; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

Qy 3 GGVPGAIPEGVPGVFPYFGAGLGGALGPGKPLKPVGGLAGAGLGAFAFPAVT 62
    |||||
Db 27 GGVPGAIPEGVPGVFPYFGAGLGGALGPGKPLK-----GLGAFPAVT 74
    |||||

Qy 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGGCGVS 100
    |||||
Db 75 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGGCGVS 112
    |||||

RESULT 12
ELS_MOUSE
ID ELS_MOUSE STANDARD; PRT; 860 AA.
AC P54320;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 25-OCT-2004 (Rel. 45, last annotation update)
DS Elastin precursor (Tropoelastin).
GN Name=El;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/c; TISSUE=Lung;
RA MEDLINE=95130069; PubMed=7829060;
RA Wyder K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
RT "Use of an intron polymorphism to localize the tropoelastin gene to
RT mouse chromosome 5 in a region of linkage conservation with human
RT chromosome 7."
RL Genomics 23:125-131(1994).
CC -I- FUNCTION: Major structural protein of tissues such as aorta and

```

```

CC nuchal ligament, which must expand rapidly and recover completely.
CC -I- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
CC -I- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -I- PTM: The crosslinks are made of deaminated lys.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U08210; AAA80155.1; -.
CC PIR; A55721; EAMS.
CC MGI; MGI:95317; Eln.
CC InterPro; IPR003979; tropoelastin.
CC PRINTS; PR01500; TROP0ELASTIN.
CC Repeat; Signal; Structural protein.
CC FT SIGNAL 1 27 Potential.
CC FT CHAIN 26 860 Elastin.
CC FT DISULFID 850 855 By similarity.
CC SEQUENCE 860 AA; 71955 MW; 0C0B53AE1EDD7F1 CRC64;

Query Match
Best Local Similarity 71.9%; Score 377; DB 1; Length 860;
Matches 82; Conservative 4; Mismatches 11; Indels 16; Gaps 5;

Qy 3 GGVPGAIPEGVPGVFPYFGAGLGGALGPGKPLK-----VPGLAGNG 50
    |||||
Db 32 GAVPGGLPEGVPGVFPYFGAGLGGGAGLGGPGKPLKGTGAGPGGIGGAG 91
    |||||

Qy 51 LGAGLGAFAFPAFPP--GALVPGGVADAAAAYK--AAKAGAGLGGVPGV--GGLGV 99
    |||||
Db 92 P8AGLGAFAFPAFPGAGLALVPGGAAGAAAYKAAKAGAGLGGVPGVGGV 144
    |||||

RESULT 13
Q8C9L8 PRELIMINARY; PRT; 860 AA.
AC Q8C9L8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, last annotation update)
DS Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630042119 product:elastin, full insert sequence
DE (Elaetin).
GN Name=El;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Thymus;
RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RT Meth. Enzymol. 303:19-44(1999).
RL [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Thymus;
RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RX [3]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of

```

RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Kanno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Kanno H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwara S., Inoue K., Togawa K., Izawa M., Ohara E., Watanabe M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
Kurihara K., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ono M., Ohnato N., Okazaki Y.,
Saito R., Satoh H., Sakai C., Sakai K., Sakurame N., Sano H.,
Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uedin T.B., Tomshylyuk S., Carninci P., Prange C.,
Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Wuzny D.M., Sodergren E.C., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
Krzyniowski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[8]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK041860; BAC31084.1; -
DR EMBL: BC051649; AA51649.1; -
DR MGD: MGI:95317; Eln.
DR GO: GO:0007519; P:myogenesis; IMP.

DR GO: GO:0030833; P:regulation of actin filament polymerization; IMP.
DR GO: GO:0043149; P:stress fiber formation; IMP.
DR InterPro: IPR003979; tropoelastin.
DR PRINTS: PRO1500; TROPELASTIN.
DR SEQUENCE 860 AA; 71938 MW; 7C340F2FFDC92E5 CRC64;
SQ
Query Match 71.9%; Score 377; DB 2; Length 860;
Best Local Similarity 72.6%; Pred. No. 3, 1e-16;
Matches 82; Conservative 4; Mismatches 11; Indels 16; Gaps 5;
QY 3 GGVPGALPGGVPGVPGAGLAL--GGGALPGGKPLKP-----VGGLAGAG 50
Db 32 GAVPGALPGGVPGVPGAGLALPGGCGGALPGGKPLKPAGLGTGAGGPGGAGAG 91
QY 51 LGAGLGAFFPVTP--GALVPGGVADAAAAYK-AAAGAGLGGVPGV--GGAGV 99
Db 92 PGAGLGAFFPVTPPGAGLALPGGAGAAAAYKAAAGAGLGGVPGGV 144
RESULT 14
Q8N2G0 PRELIMINARY; PRT; 472 AA.
ID Q8N2G0;
AC Q8N2G0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein PSEC0191.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
Nagahari K., Sugano S., Isogai T.,
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK075494; BAC11651.1; -
DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO: GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro: IPR001451; Hexapep. transf.
DR InterPro: IPR003979; tropoelastin.
DR PRINTS: PRO1500; TROPELASTIN.
DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
FT NON TER 472 472
SQ SEQUENCE 472 AA; 42265 MW; 8D7A0F3A9BF971F3 CRC64;
Query Match 71.7%; Score 375.5; DB 2; Length 472;
Best Local Similarity 79.4%; Pred. No. 2, 5e-16;
Matches 77; Conservative 1; Mismatches 18; Indels 1; Gaps 1;
QY 3 GGVPGALPGGVPGVPGAGLALPGGKPLKPYPGGLAGLGGAGLGAFFAVT 62
Db 27 GGVPGALPGGVPGVPGAGLALPGGKPLKPYPGGLAGLGGAGLGGAGLGGV 86
QY 63 FPGALVPGG-VADAAAAYKAAAGAGLGGVPGVG 98
Db 87 IPGAVGAGPAAAAAAXKAAKYGAAAGLVPGGPRFG 123
RESULT 15
ID Q6ZM06 PRELIMINARY; PRT; 570 AA.
AC Q6ZM06;
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16246.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Matanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagaatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuno Y., Nagai K., Isogai T.,
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK122731; BAC85506.1; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR003979; tropoelastin.
DR InterPro; IPR001451; Hexapep_transf.
DR PRINTS; PR01500; TROPELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
SQ SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B CRC64;

Query Match 67.0%; Score 351; DB 2; Length 570;
Best Local Similarity 57.4%; Pred. No. 9.9e-15; Indels 46; Gaps 5;
Matches 81; Conservative 2; Mismatches 12;
QY 3 GGVPGAIPEGVPGGVFPYPGAGLGGALGPGKPLKPPGGLAGAGLGAFL-GAFPAY 61
Db 27 GGVPGAIPEGVPGGVFPYPGAGLGGALGPGKPLKPPGGLAGAGLGAFLGAFAFI 86
QY 62 TRPG-----ALVPGVAD-----AAAY 79
Db 87 --PGVPPFGAPQPGVPLGYPIKAPKLPGYPGGVAGAGKAGYPTGTGVPQAAAAAAAK 144
QY 80 KAAKAGAGLGV--PGVGLGV 99
Db 145 AAAKFGAGAGVLPVGGAGV 165

Search completed: August 10, 2005, 07:37:41
Job time : 113.94 secs

THIS PAGE IS BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2005, 07:16:57 ; Search time 120.095 Seconds
(without alignments)
325.267 Million cell updates/sec

Title: US-09-743-818a-4_COPY_500_600

Perfect score: 501
Sequence: 1 VAAAKSAKAAKAAKQRLAA.....QHLPSPSPRVGALAAK 101

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	100.0	730	2	AAW46315 Human ela
2	501	100.0	731	3	AAW46315 Human ela
3	501	100.0	731	4	AAW46315 Human ela
4	501	100.0	731	6	ABU08725 Human ela
5	501	100.0	731	7	ADL96420 Human ela
6	501	100.0	733	2	AAW46315 Human ela
7	501	100.0	733	2	AAW46315 Human ela
8	501	100.0	757	7	ABG75223 Human ela
9	501	100.0	757	7	ADP65160 Human ela
10	424	84.6	216	2	AAW46315 Human ela
11	308	61.5	200	2	AAW46315 Human ela
12	304.5	60.8	617	7	ADB64761 Human ela
13	304.5	60.8	660	7	AAW46315 Human ela
14	304.5	60.8	663	7	ADM03792 Human ela
15	304.5	60.8	692	7	ADW40134 Human ela
16	304.5	60.8	698	2	AAW46315 Human ela
17	304.5	60.8	698	3	AAW46315 Human ela
18	304.5	60.8	712	3	AAW46315 Human ela
19	304.5	60.8	730	3	AAW46315 Human ela
20	304.5	60.8	730	5	AAW46315 Human ela
21	304.5	60.8	730	8	ADW40134 Human ela
22	304.5	60.8	870	7	ADW40134 Human ela
23	304.5	60.8	570	8	ADW40134 Human ela
24	301.5	60.2	711	7	ADW40134 Human ela
25	300.5	60.0	472	4	AAW46315 Human ela

26	266	53.1	571	3	AAW46315 Human ela
27	249.5	49.8	864	7	ADW40134 Human ela
28	227.5	45.4	183	3	AAW46315 Human ela
29	227.5	45.4	183	3	AAW46315 Human ela
30	191	38.1	171	3	AAW46315 Human ela
31	174	34.7	34	2	AAW46315 Human ela
32	170	33.9	34	2	AAW46315 Human ela
33	159	31.7	34	1	AAW46315 Human ela
34	159	31.7	217	2	AAW46315 Human ela
35	159	31.7	281	2	AAW46315 Human ela
36	158	31.5	223	2	AAW46315 Human ela
37	158	31.5	287	2	AAW46315 Human ela
38	155	30.9	877	2	AAW46315 Human ela
39	155	30.9	877	2	AAW46315 Human ela
40	154.5	30.8	235	2	AAW46315 Human ela
41	154	30.7	244	8	ADR70475 Human ela
42	154	30.7	246	8	ADR70475 Human ela
43	154	30.7	246	8	ADR70475 Human ela
44	154	30.7	884	2	AAW46315 Human ela
45	154	30.7	884	2	AAW46315 Human ela

ALIGNMENTS

RESULT 1
ID AAW46315 standard; protein; 730 AA.
XX AAW46315;

DT 23-JUL-1998 (first entry)

DE Human elastin containing non-natural polypeptide MFU-1 sequence.

XX MFU-1; minimal functional unit; elastin; human; fibrous protein;

KW beta-sheet; coating; wound dressing.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Protein 374..499

FT /note="MFU-1 polypeptide"

XX WO9805685-A2.

PD 12-FEB-1998.

PF 07-AUG-1997; 97WO-CA000560.

PR 07-AUG-1996; 96US-0023552P.

PR 07-AUG-1997; 97US-0091364.

XX (PROT-) PROTEIN SPECIALTIES LTD.

PA (HOSP-) HOSPITAL FOR SICK CHILDREN.

XX Rothstein A, Keeley FW, Rothstein SJ;

PI WPI; 1998-145551/13.

DR New non-natural polypeptide with multiple beta-sheet, beta-turn

XX structures - particularly based on human elastin, useful for coating

PT prostheses, as wound dressings, etc., allows ingrowth of cells.

XX Claim 5; Fig 1B; 39p; English.

CC This represents the human elastin sequence containing the minimal

CC functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a

CC polypeptide that has at least 3 beta-sheet/ beta-turn structures, but is

CC not a naturally occurring fibrous protein. Each beta-sheet structure has

CC 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at

CC least 1 amino acid that can take part in crosslinking. The polypeptide

CC can also be derived from the sequences of animal elastin, lampirin and

CC spider silk protein. The MFU polypeptides are self-aligning peptides
CC having the same primary structure as part of a natural fibrous protein.
CC They are used to coat prostheses made of animal or synthetic material or
CC metal, particularly for use as blood vessel or heart valve replacements,
CC wound or burn dressings, or stents. They can be used in cosmetic, elastic
CC or high-tensile strength materials, e.g. ropes or parachute cord.
CC Prostheses based on the MFU allow penetration of endothelial cells, so
CC become permanent, living, tissue replacements. The MFU polypeptides have
CC better biocompatibility than known elastin-based materials. They are well
CC defined, homogeneous material and are easier to manipulate and produce
CC than full-length elastin. They are non-thrombogenic and non-immunogenic.
CC Materials can be made from 2 or more different MFU polypeptides to allow
CC properties to be tailored for particular applications, e.g. combining the
CC high extensibility of elastin and the high tensile strength of spider
CC silk protein

XX Sequence 730 AA;

Query Match 100.0%; Score 501; DB 2; Length 730;
Best Local Similarity 100.0%; Pred. No. 4.4e-34;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAKAQQLRAAGIGAGIPGLGVGVPGIGVGAGVPGIGAGVPGFGAG 60
DB 498 VAAAKSAKVAKAQQLRAAGIGAGIPGLGVGVPGIGVGAGVPGIGAGVPGFGAG 557

QY 61 ADEGVRRSLSPELREGDPSSQHLPTSPSSPRVPALAAAK 101
DB 558 ADEGVRRSLSPELREGDPSSQHLPTSPSSPRVPALAAAK 598

RESULT 2
AA69068
ID AAY69068 standard; protein; 731 AA.

AC AAY69068;
XX
DT 30-MAY-2000 (first entry)

DE Amino acid sequence of a human tropoelastin splice form.

XX Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
KM hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
KM peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
XX
OS Homo sapiens.

XX
XX Key Location/Qualifiers
FH Cleavage-site 441..442
FT Cleavage-site 503..504
FT Cleavage-site 515..516
FT Cleavage-site 564..565

XX WO200004043-A1.

XX 27-JAN-2000.

XX 19-JUL-1999; 99WO-AU000580.

XX 17-JUL-1998; 98AU-00004723.

XX (UNSY) UNIV SYDNEY.

XX Weiss AS;

XX WPI; 2000-182399/16.

XX N-PSDB; AA261146.

XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and

XX cell growth.

XX Disclosure; Page 107-109; 136pp; English.

CC The present sequence represents a human tropoelastin splice form. The
CC specification describes tropoelastin derivatives, in which a subsequence
CC has been mutated so that susceptibility to proteolysis is reduced or
CC eliminated, or a subsequence has been inserted so that susceptibility to
CC proteolysis is increased. The derivatives have with reduced
CC susceptibility, and can be used where the wild-type protein would be
CC degraded too easily, e.g. in contact with serum or wound exudate. The
CC tropoelastin derivatives provide competitive inhibition of protease
CC activity. The tropoelastin derivatives, and other polypeptides containing
CC tropoelastin derivative-derived protease-susceptibility sites, are useful
CC in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand
CC lotions), as bulking agents and for inducing chemotaxis. They are also
CC useful for proliferation or growth inhibition, particularly of smooth
CC muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes,
CC chondrocytes and platelets. Peptidomimetics that mimic the protease
CC cleavage site in tropoelastin derivatives are competitive inhibitors of
CC the protease, and are used for protecting against lung damage caused by
CC elastin, for inhibiting or controlling localized growth of cancers or
CC metastases, or to limit protease activity that causes blood clotting

XX Sequence 731 AA;

Query Match 100.0%; Score 501; DB 3; Length 731;
Best Local Similarity 100.0%; Pred. No. 4.4e-34;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAKAQQLRAAGIGAGIPGLGVGVPGIGVGAGVPGIGAGVPGFGAG 60
DB 498 VAAAKSAKVAKAQQLRAAGIGAGIPGLGVGVPGIGVGAGVPGIGAGVPGFGAG 557

QY 61 ADEGVRRSLSPELREGDPSSQHLPTSPSSPRVPALAAAK 101
DB 558 ADEGVRRSLSPELREGDPSSQHLPTSPSSPRVPALAAAK 598

RESULT 3
AAB6657
ID AAB6657 standard; protein; 731 AA.

AC AAB6657;

DT 05-APR-2001 (first entry)

DE Human elastin protein without signal peptide.

XX Minimal function unit; MFU; human; elastin prosthetic.

XX Homo sapiens.

XX WO200100666-A2.

XX 04-JAN-2001.

XX 29-JUN-2000; 2000WO-US017829.

XX 29-JUN-1999; 99US-00340736.

XX (PROT-) PROTEIN SPECIALTIES LTD.

XX (HSCR-) HSC RES & DEV LP.

XX Rochstein A, Keeley F, Rochstein S, Stahl R;

XX WPI; 2001-102886/11.

XX Novel polypeptides that comprise three beta-sheet/beta-turn structures

XX and are not naturally occurring fibrous protein, used to produce

XX prostheses suitable for implantation into humans, and cosmetic materials.

XX Claim 1; Fig 1; 39pp; English.

XX The present invention relates to a minimal functional unit (MFU) of human

XX elastin polypeptide. This protein is useful in a cosmetic material or a

XX prosthetic material such as prostheses for blood vessel replacements, for

CC heart valve replacement, tissue replacement, for covering burns, for
CC covering wounds and stents
XX
SQ Sequence 731 AA;
Query Match 100.0%; Score 501; DB 4; Length 731;
Best Local Similarity 100.0%; Pred. No. 4,4e-34;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VAAAKSAKVAKAQOLRAAGIGAGIPGLGVGVPGIGVAGVPGIGVAGVPGGAG 60
DB 498 VAAAKSAKVAKAQOLRAAGIGAGIPGLGVGVPGIGVAGVPGIGVAGVPGGAG 557
QY 61 ADEGVRRSLSPELREDPSSOHLPTSPSSPRVPGLAALAK 101
DB 558 ADEGVRRSLSPELREDPSSOHLPTSPSSPRVPGLAALAK 598
RESULT 4
ABU08725 100.0%; Score 501; DB 4; Length 731;
ID ABU08725 standard; protein; 731 AA.
XX
AC ABU08725;
XX
DT 25-JUN-2003 (first entry)
XX
DE Human elastin mature protein.
XX
KM Human; elastin; minimal functioning unit; MFU;
KM beta-sheet/beta-turn structure; fibrous protein; prosthesis;
KM blood vessel replacement; heart replacement valve; burn; wound; lamprin;
KM spider silk; cord; rope; parachute; cosmetic; platelet binding inhibitor;
KM platelet activation inhibitor; non-chromogenic; cell infiltration;
KM non-immunogenic; biocompatible; high tensile strength; elasticity;
KM plasticity.
XX
OS Homo sapiens.
XX
PN US6489446-B1.
XX
PD 03-DEC-2002.
XX
PF 29-JUN-1999; 99US-00340736.
XX
PR 07-AUG-1996; 96US-0023522P.
PR 07-AUG-1997; 97US-00911364.
XX
PA (HSCR-) HSC RES & DEV LP.
PA (PROT-) PROTEIN SPECIALTIES LTD.
XX
PI Rothstein A, Keeley F, Rothstein S;
XX
DR WPI; 2003-391056/37.
XX
PT Novel polypeptide useful in prosthesis, has a secondary structure
PT characterized by three beta-sheet/beta-turn structures, and is not a
PT naturally occurring fibrous protein.
XX
PS Claim 1; Fig 1B; 21pp; English.
XX
CC The invention describes a polypeptide (I) comprising a minimal
CC functioning unit (MFU) which is present in the sequence of human elastin
CC and comprised of at least three beta-sheet/beta-turn structures, and at
CC least one amino acid residue that participates in cross-linking, and not
CC a naturally occurring fibrous protein. The MFU material can be used to
CC construct human elastin-like prostheses such as tubes for blood vessel
CC replacement, heart replacement valves and sheets for other uses such as
CC burns or wounds to promote healing. MFUs can be co-aggregated with other
CC proteins, for e.g. collagen, to provide prosthesis material that
CC resembles the natural structural materials of the body. MFUs modeled on
CC lamprin and other fibrous proteins e.g. spider silk, can be used to make
CC a variety of materials, for a number of different applications, for e.g.
CC in cords and ropes for use in parachutes and in cosmetics. Coating

CC synthetic prosthesis with MFUs modeled on human elastin significantly
CC inhibits platelet binding and activation. The human-like MFU material is
CC more biocompatible than other elastin-containing materials. In contrast
CC to solubilised fragments of elastin used before, an MFU is a single
CC peptide of defined composition. The MFU is considerably smaller than the
CC parent protein, simpler in structure, easier to produce or express in
CC quantity, to handle in solution and to manipulate for experimental and
CC practical purposes. Like other elastin preparations, the MFU is non-
CC thrombogenic and provides a friendly environment for cell infiltration.
CC Being composed entirely of a human elastin sequence, MFU is non-
CC immunogenic, thus providing a truly biocompatible material. MFUs modeled
CC on lamprin and other fibrous proteins can be used to make a variety of
CC materials having high tensile strength, elasticity and plasticity of
CC their parent proteins. This is the amino acid sequence of mature human
CC elastin on which the MFU peptides of the invention are based
SQ Sequence 731 AA;
Query Match 100.0%; Score 501; DB 6; Length 731;
Best Local Similarity 100.0%; Pred. No. 4,4e-34;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VAAAKSAKVAKAQOLRAAGIGAGIPGLGVGVPGIGVAGVPGIGVAGVPGGAG 60
DB 498 VAAAKSAKVAKAQOLRAAGIGAGIPGLGVGVPGIGVAGVPGIGVAGVPGGAG 557
QY 61 ADEGVRRSLSPELREDPSSOHLPTSPSSPRVPGLAALAK 101
DB 558 ADEGVRRSLSPELREDPSSOHLPTSPSSPRVPGLAALAK 598
RESULT 5
ADL96420 100.0%; Score 501; DB 6; Length 731;
ID ADL96420 standard; protein; 731 AA.
XX
AC ADL96420;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human elastin protein fragment.
XX
KM fibrous protein; prosthesis; elastin; lamprin; spider silk protein;
KM blood vessel; wound; burn healing; collagen.
XX
OS Homo sapiens.
XX
PN US2003166846-A1.
XX
PD 04-SEP-2003.
XX
PF 28-SEP-2001; 2001US-00964662.
XX
PR 07-AUG-1996; 96US-0023522P.
PR 07-AUG-1997; 97US-00911364.
PR 29-JUN-1999; 99US-00340736.
XX
PA (ROTH/) ROTHSTEIN A.
PA (KEEL/) KEELEY F.
PA (ROTH/) ROTHSTEIN S.
XX
PI Rothstein A, Keeley F, Rothstein S;
XX
DR WPI; 2003-898105/82.
XX
FT Key Location/Qualifiers
FT Region 19..160
FT /note="region specifically claimed in claim 6"
FT Region 188..367
FT /note="region specifically claimed in claim 6"
FT Region 374..499
FT /note="region specifically claimed in claim 6"
FT Region 607..717
FT /note="region specifically claimed in claim 6"

XX polypeptide for constructing human elastin-like prostheses such as tubes
PT for blood vessel replacement and sheets for other uses such as wound or
PT burn healing, comprises three beta sheets and three beta turns.

XX Claim 5, Fig 1B; 17pp; English.

XX This invention describes a polypeptide that comprises three beta
CC sheet/beta turn structures and that is not a naturally occurring fibrous
CC protein. The invention also describes a prosthesis comprising an animal,
CC metal or synthetic material, where the surface is coated with the
CC polypeptide, a cosmetic material comprising the polypeptide, an elastic
CC material comprising the polypeptide, a high tensile strength material
CC comprising the polypeptide, a material comprising two or more
CC polypeptides selected from (a) a polypeptide consisting essentially of a
CC portion of the polypeptide comprising at least three beta sheet/beta turn
CC structures, (b) a polypeptide consisting essentially of a portion of the
CC amino acid sequence of an animal elastin comprising at least three beta
CC sheets/beta turns, (c) a polypeptide consisting essentially of a portion
CC of lamprin comprising at least three beta sheets/beta turns, and (d) a
CC polypeptide consisting essentially of a spider silk protein comprising at
CC least three beta sheets/beta turns; a polypeptide having the primary
CC structure of a portion of a naturally occurring fibrous protein and a
CC secondary structure comprising at least three beta sheets/beta turns,
CC where each of the beta sheet/beta turn structures comprises from 3 to
CC about 7 amino acids and the polypeptide is not a naturally occurring
CC fibrous protein. The minimal functional unit (MFU) of the invention is
CC useful to construct human elastin-like prostheses such as tubes for blood
CC vessel replacement and sheets for other uses such as wound or burn
CC healing. Alternatively the MFU can be co-aggregated with other proteins,
CC for example collagen, to provide prosthesis material that resembles the
CC natural structural materials of the body. The MFU based material is
CC subject to infiltration of cells growing in the patient, including
CC endothelial cells, and the prosthesis can become a permanent living
CC tissue replacement. The material is more biocompatible than other elastin
CC -containing materials proposed for prostheses.

XX Sequence 731 AA;

XX Query Match 100.0%; Score 501; DB 7; Length 731;

XX Best Local Similarity 100.0%; Pred. No. 4,4e-34;

XX Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 VAAAKSAKVAKAAQLRAAGAGAGIPGLGVGVPGIGVAGVPGFAG 60

XX 498 VAAAKSAKVAKAAQLRAAGAGAGIPGLGVGVPGIGVAGVPGFAG 557

XX QY 61 ADEGVRRLSPELREGDPSSQHLPTSPSSPRVPALAAK 101

XX 558 ADEGVRRLSPELREGDPSSQHLPTSPSSPRVPALAAK 598

XX Db

XX RESULT 6

XX AARS6653

XX ID AARS6653 standard; protein; 733 AA.

XX AC AARS6653;

XX XX 25-MAR-2003 (revised)

XX DT 22-MAR-1995 (first entry)

XX XX Synthetic human tropoelastin (SHEL).

XX DE Tropoelastin; pharmaceutical; surgical dressing.

XX KM Synthetic.

XX OS WO9414958-A1.

XX PN 07-JUL-1994.

XX PD 16-DEC-1993; 93WO-AU000655.

PR 22-DEC-1992; 92AU-00006520.

PR 28-JUN-1993; 93AU-00009661.

XX (UNSY) UNIV SYDNEY.

XX PI Weiss AS, Martin SL;

XX DR WPI; 1994-263633/32.

XX DR N-PSDB; AAQ70941.

XX PT Synthetic polynucleotide(s) - encode recombinant tropoelastins and

XX variants.

XX PS Disclosure; Page 30; 77pp; English.

XX CC Human synthetic tropoelastin is susceptible to hydrolytic breakdown of

XX the crosslinks. Such material may be useful in e.g. surgical

XX applications, where the gradual loss of material over time is intended.

XX CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 731 AA;

XX Query Match 100.0%; Score 501; DB 2; Length 733;

XX Best Local Similarity 100.0%; Pred. No. 4,4e-34;

XX Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 VAAAKSAKVAKAAQLRAAGAGAGIPGLGVGVPGIGVAGVPGFAG 60

XX 500 VAAAKSAKVAKAAQLRAAGAGAGIPGLGVGVPGIGVAGVPGFAG 559

XX QY 61 ADEGVRRLSPELREGDPSSQHLPTSPSSPRVPALAAK 101

XX 560 ADEGVRRLSPELREGDPSSQHLPTSPSSPRVPALAAK 600

XX Db

XX RESULT 7

XX AAY01301

XX ID AAY01301 standard; protein; 733 AA.

XX AC AAY01301;

XX XX 07-JUN-1999 (first entry)

XX DT Amino acid sequence of synthetic human tropoelastin SHEL.

XX DE Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;

XX KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;

XX XX hand lotion; surgical implant; industrial product; human; SHEL.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO903886-A1.

XX PD 28-JAN-1999.

XX PF 17-JUL-1998; 98WO-AU000564.

XX PR 18-JUL-1997; 97AU-00008117.

XX PA (UNSY) UNIV SYDNEY.

XX PI Weiss AS;

XX DR WPI; 1999-132162/11.

XX DR N-PSDB; AAX27704.

XX PT New derivatives of human tropoelastin - with elastin-like or

XX macromolecular binding properties, useful e.g. as surgical implants.

XX PS Disclosure; Fig 1; 82pp; English.

XX CC The invention relates to a derivative or variant of human tropoelastin

CC	actin ratio in a smooth muscle cell, treating or preventing obstructive
CC	vascular disease (e.g. restenosis following angioplasty), or preventing
CC	stenosis. It is also useful in manufacturing a medicament for the
CC	treatment or prevention of occlusion of a vessel. The present sequence is
CC	the human tropoelastin protein as shown in the exemplification of the
CC	invention
XX	
XX	Sequence 757 AA;
XX	
XX	Query Match 100.0%; Score 501, DB 7; Length 757;
XX	Best Local Similarity 100.0%; Pred. No. 4,6e-34;
XX	Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	
Db	1 VAAAKSAAKVAAKAAQQLRAAAGLGAGIPGLGVGVPGELGVGAGVPGAGVPGFAG 60
	524 VAAAKSAAKVAAKAAQQLRAAAGLGAGIPGLGVGVPGELGVGAGVPGAGVPGFAG 583
QY	61 ADEGVRRSLSPELRECGDPSSSQHLPTSPSSPRVPGALAAAK 101
Db	584 ADEGVRRSLSPELRECGDPSSSQHLPTSPSSPRVPGALAAAK 624
RESULT 9	
ID	ADP65160
XX	ADP65160 standard; protein; 757 AA.
XX	
XX	ADP65160;
XX	
D7	12-AUG-2004 (first entry)
XX	
DE	Human elastin.
XX	
XX	autoimmune disease; arthritide; gene expression analysis;
KW	rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW	antiarthritis; osteopathic; antigout; antiinflammatory; dermatological;
KW	immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
KW	fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW	immune; human.
XX	
XX	Homo sapiens.
OS	
PN	MO2003072827-A1.
PD	04-SEP-2003.
XX	
XX	31-OCT-2002; 2002WO-US035433.
XX	
XX	31-OCT-2001; 2001US-0336220P.
XX	
PA	(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX	
PI	Hirsch R, Thornton SL;
XX	
DR	WPI; 2003-712740/67.
XX	
DR	GENBANK; NP_000442.
XX	
PT	Diagnosing and analyzing autoimmune disease using gene expression
PT	profiles and microarray technology, useful for diagnosing and treating
PT	rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT	gout.
XX	
XX	Disclosure; Page; 56pp; English.
XX	
XX	The invention relates to a novel method for diagnosing and analysing
CC	autoimmune disease or arthritides. The method comprises obtaining a
CC	patient sample containing mRNA, analysing gene expression using the mRNA
CC	that results in a gene expression signature of the mRNA, and using that
CC	gene expression signature to diagnose or analyse the autoimmune disease
CC	or arthritides in the patient, where gene expression of at least 60% of
CC	the genes correlates with that of the gene signature. The invention
CC	further comprises: a treatment of rheumatoid arthritis; identification of
CC	genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC	other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an

CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC antipain, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritis, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This sequence represents a
CC protein sequence relating to the genes used in the analysis and treatment
CC of autoimmune diseases or arthritis. Note: This sequence is not shown
CC in the specification. It has been supplied in an electronic format from
CC WIPO.

SQ Sequence 757 AA;
Query Match 100.0%; Score 501; DB 7; Length 757;
Best Local Similarity 100.0%; Pred. No. 4.6e-34;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAQAQLRRAAGIGAGIPGLGVGVPGLVGAGVPGFAG 60
DB 524 VAAAKSAKVAQAQLRRAAGIGAGIPGLGVGVPGLVGAGVPGFAG 583
QY 61 ADEGVRRSLSPRLREGDPSSQHLPTSPSSPRVPGALAAK 101
DB 584 ADEGVRRSLSPRLREGDPSSQHLPTSPSSPRVPGALAAK 624

RESULT 10
AA01310
ID AA01310 standard; protein; 216 AA.
XX
XX AA01310;
XX
DT 07-JUN-1999 (first entry)
XX
DE Human tropoelastin derivative SHEL26-36.
XX
XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
XX
XX Homo sapiens.
OS Synthetic.
OS
PN WO903886-A1.
XX
PD 28-JAN-1999.
XX
PF 17-JUL-1998; 98WC-AU000564.
XX
PR 18-JUL-1997; 97AU-00008117.
XX
PA (UNSY) UNITV SYDNEY.
XX
XX Weiss AS;
PI
XX
XX MPI; 1999-132162/11.
XX
PT New derivatives of human tropoelastin - with elastin-like or
XX macromolecular binding properties, useful e.g. as surgical implants.
XX
XX Claim 35; Page 11; 82pp; English.
XX
XX The invention relates to a derivative or variant of human tropoelastin
CC (hTE) having elastin-like and/or macromolecule (specifically
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
CC comprising the nucleic acids encoding the variants or derivatives are
CC used to produce the proteins recombinantly. The tropoelastin derivatives

CC or hybrid proteins containing the derivatives are useful in medical,
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
CC wrinkle or hand lotions, also as surgical implants, foods and industrial
CC products. The hybrid protein have controllable GAG-binding properties,
CC depending on presence or absence of a specific fragment, designated
CC peptide 26a, from hTE. The present sequence represents a human
CC tropoelastin derivative SHEL26-36

SQ Sequence 216 AA;
Query Match 84.6%; Score 424; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 4.2e-28;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 AAAGGAGIPGLGVGVPGLVGAGVPGFAGADGVRRSLSPRLREGDP 78
DB 1 AAAGGAGIPGLGVGVPGLVGAGVPGFAGADGVRRSLSPRLREGDP 60
QY 79 SSSQHLPTSPSSPRVPGALAAK 101
DB 61 SSSQHLPTSPSSPRVPGALAAK 83

RESULT 11
AA01305
ID AA01305 standard; protein; 200 AA.
XX
XX AA01305;
XX
DT 07-JUN-1999 (first entry)
XX
DE Human tropoelastin derivative SHELgamma.
XX
XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
XX
XX Homo sapiens.
OS Synthetic.
OS
PN WO903886-A1.
XX
PD 28-JAN-1999.
XX
PF 17-JUL-1998; 98WC-AU000564.
XX
PR 18-JUL-1997; 97AU-00008117.
XX
PA (UNSY) UNITV SYDNEY.
XX
XX Weiss AS;
PI
XX
XX MPI; 1999-132162/11.
XX
PT N-PSDB; AA027707.
XX
XX New derivatives of human tropoelastin - with elastin-like or
XX macromolecular binding properties, useful e.g. as surgical implants.
XX
XX Claim 15; Fig 8; 82pp; English.
XX
XX The invention relates to a derivative or variant of human tropoelastin
CC (hTE) having elastin-like and/or macromolecule (specifically
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
CC comprising the nucleic acids encoding the variants or derivatives are
CC used to produce the proteins recombinantly. The tropoelastin derivatives
CC or hybrid proteins containing the derivatives are useful in medical,
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
CC wrinkle or hand lotions, also as surgical implants, foods and industrial
CC products. The hybrid protein have controllable GAG-binding properties,
CC depending on presence or absence of a specific fragment, designated
CC peptide 26a, from hTE. The present sequence represents a human
XX tropoelastin derivative SHELgamma

```

CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
CC XX
XX Sequence 617 AA;
SQ
Query Match      60.8%; Score 304.5; DB 7; Length 617;
Best Local Similarity 67.3%; Pred. No. 1.4e-17;
Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;
OY 1 VAAAKSAKAYAAQAOLRAAAGLGAAGIPGLGVGVGVLGGVAGACVPGLGVAGAVPGFAG 60
Db 435 VAAAKSAKAYAAQAOLRAAAGLGAAGIPGLGVGVGVLGGVAGACVPGLGVAGAVPGFAGA- 493
OY 61 ADEGVRRSLSPELREBDDPSSQHLPTSPSPRPVGAIAAK 101
Db 494 -----VPGALAAAK 502
RESULT 13
ID AAY01303 standard; protein; 660 AA.
XX AC AAY01303;
XX AC AAY01303;
DT 07-JUN-1999 (first entry)
XX DE Human tropoelastin derivative SHRLdeltaIamodified.
XX KW Tropoelastin; hME; elastin; glycosaminoglycan; GAG-binding; medical;
XX pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
XX hand lotion; surgical implant; industrial product; human; SHRL.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO9903886-A1.
XX PD 28-JAN-1999.
XX PF 17-JUL-1998; 98WO-AU000564.
XX PR 18-JUL-1997; 97AU-00008117.
XX PA (UNSY ) UNIV SYDNEY.
XX PI Weiss AS;
XX WP1; 1999-132162/11.
XX DR N-PsDB; AAX27705.
XX PT New derivatives of human tropoelastin - with elastin-like or
XX macromolecular binding properties, useful e.g. as surgical implants.
XX PS Claim 7; Fig 3; 82pp; English.
XX CC The invention relates to a derivative or variant of human tropoelastin
(hME) having elastin-like and/or macromolecule (specifically
glycosaminoglycan (GAG))-binding properties. Cells containing vectors
comprising the nucleic acids encoding the variants or derivatives are
used to produce the proteins recombinantly. The tropoelastin derivatives
or hybrid proteins containing the derivatives are useful in medical,
pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
wrinkle or hand lotions, also as surgical implants, foods and industrial
products. The hybrid protein have controllable GAG-binding properties,
depending on presence or absence of a specific fragment, designated
peptide 26A, from hME. The present sequence represents a human
tropoelastin derivative SHRLdeltaIamodified

```


PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.

PS Claim 1; SEQ ID NO 40; 560pp; English.

XX
XX
CC The invention relates to a novel NOVX polypeptide. The polypeptide of the
CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,
CC cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,
CC neuroprotective, nootropic, antiparkinsonian, antiasthmatic and
CC gynaecological activities and may be useful in diagnosing, treating or
CC preventing NOVX-associated disorders including cardiomyopathy,
CC atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple
CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's
CC disease, asthma or fertility disorders. Furthermore, the polypeptides may
CC be utilised as vaccines whilst the nucleic acids may be used as
CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,
CC preventive medicine and pharmacogenomics. The current sequence is that of
CC the human NOV protein of the invention.

XX
SQ Sequence 692 AA;

Query Match 60.8%; Score 304.5; DB 7; Length 692;

Best Local Similarity 67.3%; Pred. No. 1.6e-17;

Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 VAAAKSAKVAQAQIRAAAGLQAGIPGLGVGVGPGLVGAAGVPGAGVPGFGAG 60

Db 492 VAAAKSAKVAQAQIRAAAGLQAGIPGLGVGVGPGLVGAAGVPGAGVPGFGA- 550

QY 61 ADEGVRRSLSPELAREGDPSSQHLPTPTSSPRYPGALAANK 101

Db 551 -----VPGALAANK 559

Search completed: August 10, 2005, 07:33:50
Job time : 120.095 secs

THIS PAGE IS BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: August 10, 2005, 07:27:07 ; Search time 30.1493 Seconds

(Without alignments)
250.074 Million cell updates/sec

Title: US-09-743-818a-4_COPY_500_600

Perfect score: 501
1 VAAAKSAKAAKAAKAAQLRAA.....QHLPSPSPRYGALAAK 101

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	100.0	731	2	US-08-911-364-1
2	501	100.0	731	4	US-09-340-736E-1
3	501	100.0	731	4	US-09-964-662-1
4	501	100.0	731	3	US-08-464-700-2
5	501	100.0	792	2	US-08-678-039A-40
6	304.5	60.8	730	4	US-09-961-403-8
7	159	31.7	281	1	US-08-397-633A-75
8	158	31.5	287	1	US-08-397-633A-76
9	155	30.9	877	1	US-08-397-633A-54
10	154	30.7	884	1	US-08-397-633A-68
11	154	30.7	884	2	US-08-435-641-15
12	154	30.7	884	2	US-08-707-237A-96
13	154	30.7	884	3	US-08-642-246-15
14	154	30.7	884	4	US-09-451-206-15
15	154	30.7	884	5	PCT-US96-06229-15
16	153	30.5	768	3	US-08-806-029-35
17	153	30.5	889	3	US-08-806-029-19
18	153	30.5	1011	1	US-08-477-509B-94
19	153	30.5	1011	3	US-08-482-085B-94
20	153	30.5	1011	3	US-09-444-791A-94
21	153	30.5	1170	1	US-08-175-155-59
22	153	30.5	1170	2	US-08-175-155-59
23	153	30.5	1170	2	US-08-175-155-59
24	153	30.5	2055	1	US-08-477-509B-81
25	153	30.5	2055	2	US-08-477-509B-81
26	153	30.5	2055	3	US-08-482-085B-81
27	153	30.5	2055	3	US-09-444-791A-81

28	153	30.5	2257	1	US-08-175-155-47	Sequence 47, Appl
29	153	30.5	2257	1	US-08-477-509B-82	Sequence 82, Appl
30	153	30.5	2257	2	US-08-707-237A-53	Sequence 53, Appl
31	153	30.5	2257	3	US-08-482-085B-82	Sequence 82, Appl
32	153	30.5	2257	3	US-09-444-791A-82	Sequence 82, Appl
33	151	30.1	479	1	US-08-397-633A-73	Sequence 73, Appl
34	151	30.1	479	1	US-08-397-633A-78	Sequence 78, Appl
35	151	30.1	750	3	US-08-806-029-25	Sequence 25, Appl
36	150	29.9	378	2	US-08-707-237A-104	Sequence 104, Appl
37	150	29.9	378	2	US-08-642-246-26	Sequence 26, Appl
38	150	29.9	378	4	US-09-451-206-26	Sequence 26, Appl
39	150	29.9	378	5	PCT-US96-06229-26	Sequence 26, Appl
40	150	29.9	486	1	US-08-397-633A-77	Sequence 77, Appl
41	150	29.9	696	3	US-08-806-029-36	Sequence 36, Appl
42	150	29.9	1002	2	US-08-707-237A-103	Sequence 103, Appl
43	150	29.9	1002	3	US-08-642-246-25	Sequence 25, Appl
44	150	29.9	1002	4	US-09-451-206-25	Sequence 25, Appl
45	150	29.9	1002	5	PCT-US96-06229-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-911-364-1

Sequence 1, Application US/08911364

Patent No. 5969106

GENERAL INFORMATION:

APPLICANT: ROTHSTEIN, Aaser

APPLICANT: KEELY, Fred W.

TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELLED ON HUMAN

TITLE OF INVENTION: ELASTIN AND OTHER FIBROUS PROTEINS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/911,364

FILING DATE: 07-AUG-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/023,552

FILING DATE: 07-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 041082/0104

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 731 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-911-364-1

Query Match 100.0%; Score 501; DB 2; Length 731;

Best Local Similarity 100.0%; Pred. No. 2,2e+11;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match	100.0%;	Score 501;	DB 4;	Length 731;
Best Local Similarity	100.0%;	Pred. No. 2.2e-41;		
Matches 101; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

	Query Match	100.0%	Score 501	DB 3	Length 733
	Best Local Similarity	100.0%	Pred. No. 2.3e-41		
	Matches 101	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Q7	1 VAAAKSAKAAKQQLPAAAGLGGIGTGLGVGVGPGGLGVGAGVPLGLGVGAGVPFGAG 60				
Db	500 VAAAKSAKAAKQQLPAAAGLGGIGTGLGVGVGPGGLGVGAGVPLGLGVGAGVPFGAG 559				
Q7	61 ADEGVRSLSPELREGDPSSOHLSTPSSPVPGLAAAK 101				
Db	560 ADEGVRSLSPELREGDPSSOHLSTPSSPVPGLAAAK 600				

RESULT 5
US-08-678-039A-40

```

; LENGTH: 730
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-403-8

Query Match
Best Local Similarity 67.3%; Score 304.5; DB 4; Length 730;
Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

Cy 1 VAAAKSAAKVAAKQLRRAAAGLGAGIPGLGVGVGVLGVGACVPGLVGAGVPGFGAG 60
|||||
Db 530 VAAAKSAAKVAAKQLRRAAAGLGAGIPGLGVGVGVLGVGACVPGLVGAGVPGFGA- 588
|||||

Cy 61 ADEGVRSLSPELRGDPSSQHLPTSPSSFRVYGALAAK 101
|||||
Db 589 -----VPGALAAK 597
|||||

RESULT 7
US-08-397-633A-75
; Sequence 75, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMTATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58648-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1969
; TELEFAX: (415) 398-3249
; TELERX: 910 277299
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-397-633A-75

Query Match
Best Local Similarity 41.7%; Score 159; DB 1; Length 281;
Matches 43; Conservative 8; Mismatches 40; Indels 12; Gaps 4;

Cy 3 AAASAARVAAKQLRRAAAGLGAGIPGLGV-----GVGVPELGV-GAGVPELGV-GAGV 54
|||||
Db 164 AGSGAGAGSGAGSGAGAGSGAGGVPGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 223
|||||

Cy 55 PGFGAGADEGVRSLSPELRGDPSSQHLPTSPSSFRVPGAL 97
|||||
Db 224 PGAGGSGAGAGSGAGAM-----DPERYMAAKQDRAPCPGGL 262
|||||

```

```

RESULT 8
US-08-397-633A-76
; Sequence 76, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
TITLE OF INVENTION: OF ENZYMAITIC CROSS-LINKING
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397, 633A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20, 015
REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-397-633A-76

Query Match          31.5%; Score 158; DB 1; Length 287;
Best Local Similarity 41.7%; Pred.No. 4.5e-08;
Matches 43; Conservative 8; Mismatches 34; Indels 18; Gaps 5

Cy      3 AAASAAKVAARQAQLPAAGLGAGIGLGV-----GVGVPGLGV-GAGVPGIGV-GAGV 54
Db      167 AGSGAGAGSAGAGAGSSAGAGSGVGIVGGVPGVGVGVGVGVGVGVGVGVGVGVGVGVGV 226
Cy      55 PGFGAGADEGVRRSLSPFLREGP-----SSQHLPSIPSSP 91
Db      227 PEGAGAGSGAGAGSGAGAM----DPGRYHMAAKGDRAFPGFPLGP 265

RESULT 9
US-08-397-633A-54
; Sequence 54, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
TITLE OF INVENTION: OF ENZYMAITIC CROSS-LINKING
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

```

/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/397,633A
/ FILING DATE:
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Rowland, Bertram I
/ REGISTRATION NUMBER: 20,015
/ REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ TELEX: 910 277299
/ INFORMATION FOR SEQ ID NO: 54:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 877 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-08-397-633A-54
/
Query Match 30.9%; Score 155; DB 1; Length 877;
Best Local Similarity 41.6%; Pred. No. 2.9e-07;
Matches 42; Conservative 8; Mismatches 33; Indels 12; Gaps 4
QY 3 AAASAAKAAKAAQILRAAAGLAGIPGLGV-----GVGVPLGLV-GAGVPLGLV-GAGV 54
DB 750 AGSGAGAGSAGAGAGAGAGAGAGSAGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGV 809
QY 55 PGFGAGADEGVRRSLSPELREGDPSSGHLSTPSSPRVPG 95
DB 810 PGAGAGSAGAGSAGAGAM----DPGRYMAAKGDRAPGTPG 846
/
RESULT 10
US-08-397-633A-68
/ Sequence 68, Application US/08397633A
/ Patent No. 5773577
/ GENERAL INFORMATION:
/ APPLICANT: Cappello, Joseph
/ TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
/ TITLE OF INVENTION: OF ENZYMAITC CROSS-LINKING
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
/ STREET: 4 Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-4187
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/397,633A
/ FILING DATE:
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Rowland, Bertram I
/ REGISTRATION NUMBER: 20,015
/ REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ TELEX: 910 277299
/ INFORMATION FOR SEQ ID NO: 68:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 884 amino acids
/

```


TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 884 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06229-15

Query Match 30.7%; Score 154; DB 5; Length 884;
Best Local Similarity 45.7%; Pred. No. 3.7e-07;
Matches 42; Conservative 7; Mismatches 31; Indels 12; Gaps 4;

QY	3	AAAKSAKVAAKQLRAAGLGGIPIGLGV-GVGVPGLGV-----GAGVPGGLGV-GAGV	54
Db	791	AGSGAGAGSGAGAGSGAGSGAGSGVGPVGVPVGKGVPGVGPVGVPVGVPVGVPVGVPVGVP	850
QY	55	PGFGAGADBGVRRSLSPELREGDPSSQLPS	86
Db	851	PGAGAGSGAGAGSGAGAM---DPGRYQDLRS	878

Search completed: August 10, 2005, 07:39:41
Job time : 31.1493 secs

THIS PAGE IS BLANK

	Score	Match Length	DB	LD	Description
0.					
1	501	100.0	731	10	US-09-964-662-1
2	490	97.8	788	16	US-10-852-665-4
3	490	97.8	788	16	US-10-852-665-3
4	304.5	60.8	617	15	US-10-104-047-2915
5	304.5	60.8	662	15	US-10-108-602-2477
6	304.5	60.8	693	15	US-10-210-172-40
7	304.5	60.8	730	10	US-09-961-403-8
8	304.5	60.8	730	16	US-10-723-660-2566
9	301.5	60.2	711	15	US-10-210-172-38
10	154	30.7	244	16	US-10-800-179-27
11	154	30.7	244	16	US-10-845-775A-27

12	154	30.7	244	15	US-10-845-936A-27	Sequence 27, Appl
13	154	30.7	244	16	US-10-939-036-27	Sequence 27, Appl
14	154	30.7	246	16	US-10-800-179-26	Sequence 26, Appl
15	154	30.7	246	16	US-10-800-179-26	Sequence 26, Appl
16	154	30.7	246	16	US-10-845-775A-26	Sequence 26, Appl
17	154	30.7	246	16	US-10-845-775A-28	Sequence 28, Appl
18	154	30.7	246	16	US-10-845-936A-26	Sequence 26, Appl
19	154	30.7	246	16	US-10-845-936A-28	Sequence 28, Appl
20	154	30.7	246	18	US-10-939-036-28	Sequence 28, Appl
21	154	30.7	246	18	US-10-939-036-28	Sequence 28, Appl
22	154	30.7	884	14	US-10-117-931-15	Sequence 15, Appl
23	154	30.7	983	16	US-10-845-936A-37	Sequence 37, Appl
24	154	30.7	1027	16	US-10-845-936A-32	Sequence 32, Appl
25	154	30.7	1105	16	US-10-845-936A-33	Sequence 33, Appl
26	154	30.7	1125	16	US-10-845-936A-34	Sequence 34, Appl
27	153	30.5	768	8	US-08-806-029-35	Sequence 35, Appl
28	153	30.5	884	16	US-10-800-179-25	Sequence 25, Appl
29	153	30.5	884	16	US-10-845-775A-25	Sequence 25, Appl
30	153	30.5	884	16	US-10-845-936A-25	Sequence 25, Appl
31	153	30.5	884	18	US-10-939-036-25	Sequence 25, Appl
32	153	30.5	889	8	US-08-806-029-19	Sequence 19, Appl
33	153	30.5	965	16	US-10-800-179-31	Sequence 31, Appl
34	153	30.5	965	16	US-10-845-775A-31	Sequence 31, Appl
35	153	30.5	965	16	US-10-845-936A-31	Sequence 31, Appl
36	153	30.5	965	18	US-10-939-036-31	Sequence 31, Appl
37	153	30.5	1011	14	US-10-096-986-34	Sequence 34, Appl
38	153	30.5	1038	16	US-10-800-179-30	Sequence 30, Appl
39	153	30.5	1038	16	US-10-845-775A-30	Sequence 30, Appl
40	153	30.5	1038	16	US-10-845-936A-30	Sequence 30, Appl
41	153	30.5	1038	18	US-10-939-036-30	Sequence 30, Appl
42	153	30.5	1055	14	US-10-096-986-31	Sequence 31, Appl
43	153	30.5	2257	14	US-10-096-986-82	Sequence 82, Appl
44	151	29.9	750	8	US-08-806-029-25	Sequence 25, Appl
45	150	29.9	378	14	US-10-117-931-26	Sequence 26, Appl

ALIGNMENTS

```

RESULT 1
US-09-964-662-1
: Sequence 1, Application US/09964662
: Publication No. US20030166846A1
: GENERAL INFORMATION:
: APPLICANT: PROTEIN SPECIALTIES LTD.
: APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
: TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELLED ON HUMAN ELASTIN AND
: TITLE OF INVENTION: OTHER FIBROUS PROTEINS
: FILE REFERENCE: 041082/012
: CURRENT APPLICATION NUMBER: US/09/964,662
: CURRENT FILING DATE: 2003-05-08
: PRIOR APPLICATION NUMBER: 09/340,736
: PRIOR FILING DATE: 1999-06-29
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 731
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-964-662-1

```

Query Match	100.0%;	Score 501;	DB 10;	Length 731;
Best Local Similarity	100.0%;	Pred. No. 2.5e-35;		
Matches 101;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps

QY VAAAKAAKAAVAAKAAQOLPAAAGIGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVGVFGAG 60
I
Db VAAAKAAKAAVAAKAAQOLPAAAGIGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVGVFGAG 55
498
QY ADEGVRRLSPRLREGDPSSSQHLPEPTSPSPVPALAAK 101
Db ADEGVRRLSPRLREGDPSSSQHLPEPTSPSPVPALAAK 598

```
RESULT 2
US-10-852-065-4
; Sequence 4, Application US/10852065
; Publication No. US20040253220A1
; GENERAL INFORMATION:
; APPLICANT: PERRIER, Eric
; APPLICANT: CENIZO, Val,rie
; APPLICANT: BOUEZ, Charbel
; APPLICANT: SOMMER, Pascal
; APPLICANT: DAMOUR, Odile
; APPLICANT: GLEYZAL, Claudine
; APPLICANT: ANDRE, Val,rie
; APPLICANT: REYMERMIER, Corinne
; TITLE OF INVENTION: Stimulation of the synthesis and of the activity of an isoform
; TITLE OF INVENTION: of lysyl oxidase-like LOXL for stimulating the formation of
; FILE REFERENCE: 11123.81US01
; CURRENT APPLICATION NUMBER: US/10/852,065
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: FR 03 07177
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-852-065-4

Query Match          97.8%; Score 490; DB 16; Length 788;
Best Local Similarity 98.1%; Pred. No. 2,4e-34;
Matches 101; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGA- 59
    VAAAAAAAAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGAV 612
DB 553 VAAAAAAAAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGA- 612
    VAAAAAAAAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGAV 612
QY 60 -GADEGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAK 101
    |||||||
DB 613 PGADGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAK 655
    |||||||

RESULT 3
US-10-852-575-3
; Sequence 3, Application US/10852575
; Publication No. US20040258676A1
; GENERAL INFORMATION:
; APPLICANT: PERRIER, Eric
; APPLICANT: BOUEZ, Charbel
; APPLICANT: CENIZO, Valerie
; APPLICANT: SOMMER, Pascal
; APPLICANT: DAMOUR, Odile
; APPLICANT: GLEYZAL, Claudine
; APPLICANT: ANDRE, Valerie
; APPLICANT: REYMERMIER, Corinne
; APPLICANT: ONLY, Isabelle
; TITLE OF INVENTION: Stimulation of the activity of an isoform of lysyl oxidase
; TITLE OF INVENTION: for combating against some pathologies due to an incomplete,
; FILE REFERENCE: 11123.82US01
; CURRENT APPLICATION NUMBER: US/10/852,575
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: FR 03 07178
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-852-575-3
```

```
Query Match          97.8%; Score 490; DB 16; Length 788;
Best Local Similarity 98.1%; Pred. No. 2,4e-34;
Matches 101; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGA- 59
    VAAAAAAAAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGAV 612
DB 553 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGA- 612
    VAAAAAAAAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGAV 612
QY 60 -GADEGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAK 101
    |||||||
DB 613 PGADGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAK 655
    |||||||

RESULT 4
US-10-104-047-2915
; Sequence 2915, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2915
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2915

Query Match          60.8%; Score 304.5; DB 15; Length 617;
Best Local Similarity 67.3%; Pred. No. 2,5e-18;
Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGA- 60
    VAAAAAAAAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGA- 493
DB 435 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGA- 493
    VAAAAAAAAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGA- 493
QY 61 ADEGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAK 101
    |||||||
DB 494 -----VPGALAAK 502
    |||||||

RESULT 5
US-10-108-260A-2477
; Sequence 2477, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2477
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2477

Query Match          60.8%; Score 304.5; DB 15; Length 663;
Best Local Similarity 67.3%; Pred. No. 2,7e-18;
Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGA- 60
    VAAAAAAAAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGA- 521
DB 463 VAAAKSAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGA- 521
    VAAAAAAAAKVAAKQOLRAAGIGAGIPGLGVGVPGIGVGAGVPGGLGVGAGVPGFGA- 521
QY 61 ADEGVRRLSPELREGDPSSSOHLPTPSSPRVPGALAAK 101
    |||||||
```


Best Local Similarity 67.3%; Pred. No. 3e-18;
Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;
QY 1 VAAAKSAKVAAKQLRRAAGLGGIPGLGVGVPGVGAGVPGVGAGVPGFAG 60
DB 530 VAAAKSAKVAAKQLRRAAGLGGIPGLGVGVPGVGAGVPGVGAGVPGFAG - 588
QY 61 ADEGVRSLSPELREGDPSSQHLPTSPSPRPVPGALAAK 101
DB 589 -----VPGALAAK 597
RESULT 9
US-10-210-172-38
; Sequence 38, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Paturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shimkets, Richard
; APPLICANT: Zernusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Mario
; APPLICANT: Vernet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjalte, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
; APPLICANT: Edinger, Shlomit
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyskay, Uriel
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Alsodrook II, John
; APPLICANT: Lepley, Denise et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-416 A
; CURRENT APPLICATION NUMBER: US/10/210,172
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327

; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 38
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-172-38
Query Match 60.2%; Score 301.5; DB 15; Length 711;
Best Local Similarity 66.3%; Pred. No. 5.3e-18;
Matches 67; Conservative 1; Mismatches 0; Indels 33; Gaps 1;
QY 1 VAAAKSAKVAAKQLRRAAGLGGIPGLGVGVPGVGAGVPGVGAGVPGFAG 60
DB 529 VAAAKSAKVAAKQLRRAAGLGGIPGLGVGVPGVGAGVPGVGAGVPGFAG - 587
QY 61 ADEGVRSLSPELREGDPSSQHLPTSPSPRPVPGALAAK 101
DB 588 -----VPGALAAK 596
RESULT 10
US-10-800-179-27
; Sequence 27, Application US/10800179
; Publication No. US20040180027A1
; GENERAL INFORMATION:
; APPLICANT: Cuevas, William A.
; APPLICANT: Kumar, Manoj
; TITLE OF INVENTION: Use of Repeat Sequence Protein Polymers in Personal Care
; FILE REFERENCE: DOC 0057 PA / GC792-4 / DC 5074
; CURRENT APPLICATION NUMBER: US/10/800,179
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/454,077
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: SEMP 47K-3
US-10-800-179-27
Query Match 30.7%; Score 154; DB 16; Length 244;
Best Local Similarity 45.7%; Pred. No. 1.2e-05;
Matches 42; Conservative 7; Mismatches 31; Indels 12; Gaps 4;
QY 3 AAKSAKVAAKQLRRAAGLGGIPGLGV-GVGVPGIGV-----GAGVPGIGV-GAGV 54
DB 151 AGSAGAGSGAGAGAGAGAGSGVGVPGVGVPGKGVGVGVPGVGVPGV 210
QY 55 PGFGAGADGCVRRSLSPELREGDPSSQHLPS 86
DB 211 PGAGAGSGAGAGAGAGAM----DPGRYDRLS 238
RESULT 11
US-10-845-775A-27
; Sequence 27, Application US/10845775A
; Publication No. US20040228913A1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Manoj
; APPLICANT: Mazeaud, Isabelle
; APPLICANT: Christiano, Steven P.
; TITLE OF INVENTION: Controlled Release of Active Agents Utilizing Repeat Sequence
; FILE REFERENCE: DOC 0077 PA/GC 792-6/DC 5110
; CURRENT APPLICATION NUMBER: US/10/845,775A
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/470,465
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 31

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2005, 07:25:52 ; Search time 24.6219 Seconds
(without alignments)
394.685 Million cell updates/sec

Title: US-09-743-818A-4_COPY_500_600
Perfect score: 501
Sequence: 1 VAAAKSAKAVAAKQALRAA.....QHLPSTPSPRPVCAALAAK 101

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	100.0	792	1 EAHU	elastin precursor,
2	265	52.9	860	1 EAMS	elastin precursor
3	254.5	52.8	747	1 EABO	elastin precursor,
4	249.5	49.8	864	1 EART	elastin precursor
5	231	46.1	770	2 SS9623	tropoelastin - she
6	154.5	30.8	784	2 A26601	elastin precursor
7	135.5	27.0	76	2 A5885	elastin - bovine (
8	130	25.9	907	2 A45560	sporozoite surface
9	117	23.4	1596	2 A33106	neurogenic locus m
10	112.5	22.5	127	2 E82734	hypothetical prote
11	109.5	21.9	505	2 T04143	CUB1 protein - tom
12	109	21.0	532	2 T35119	probable aminotran
13	105	21.0	1329	2 T29074	hypothetical prote
14	104	20.8	151	2 T08002	glycine-rich prote
15	103.5	20.7	108	2 G86252	hypothetical prote
16	103.5	20.7	185	2 UC4085	glycine-rich cutic
17	103	20.6	100	2 T17558	glycine-rich prote
18	102.5	20.5	129	2 T17530	glycine-rich prote
19	100	20.0	419	2 G70602	hypothetical prote
20	99.5	19.9	130	2 T04048	hypothetical prote
21	99.5	19.9	1901	2 T70806	hypothetical glyci
22	99	19.8	108	2 S01844	fibroin - silkworm
23	99	19.8	447	2 G84687	probable disease r
24	98.5	19.7	158	2 T08957	glycine-rich prote
25	98.5	19.7	1240	2 T04193	hypothetical prote
26	98	19.6	143	2 SA3071	hypothetical prote
27	98	19.6	1147	2 MMAX1B	myosin heavy chain
28	97.5	19.5	1733	1 B45344	probable nuclear a
29	97.5	19.5	1958	2 B40505	hypothetical prote

30	96.5	19.3	107	2 B85356	glycine-rich prote
31	96.5	19.3	149	2 T18758	hypothetical prote
32	96.5	19.3	554	1 P2WL41	I2 protein - human
33	96.5	19.3	671	2 A35912	homeotic protein o
34	96	19.2	162	2 C85356	glycine-rich prote
35	95.5	19.1	212	2 E86179	hypothetical prote
36	95	19.0	223	2 B96506	hypothetical prote
37	95	19.0	490	2 T09084	phosphatidylinosit
38	95	19.0	754	2 A55267	collagen alpha 5(I
39	95	19.0	1758	2 T29350	hypothetical prote
40	95	19.0	1759	2 T29351	collagen alpha 2(I
41	94.5	18.9	162	2 S56703	glycine-rich cell
42	94.5	18.9	171	2 T43959	hypothetical prote
43	94.5	18.9	459	2 T35317	probable serine/th
44	94.5	18.9	838	2 AC1064	outer membrane fin
45	94	18.8	208	2 S23463	cuticular protein

ALIGNMENTS

RESULT 1

EAHU
elastin precursor, long splice form - human
N/Alternate names: tropoelastin

C/Species: Homo sapiens (man)
C/Date: 22-Jun-1990 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C/Accession: A32707; A33705; A30524; A53891
R/Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenblum, J

Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987

A/Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of c

A/Reference number: A32707; MUID:87289668; PMID:3039501

A/Accession: A32707

A/Residues: 1-500,507-792 <IND>

A/Cross-references: UNIPROT:P15502; UNIPROT:Q9UMK5; GB:M16983; GB:J02948
R/Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenblum, J. C.; Abrams, W

J. Biol. Chem. 264, 8887-8891, 1989

A/Title: Characterization of the complete human elastin gene. Delineation of unusual fe

A/Reference number: A33705; MUID:89255358; PMID:2722804

A/Accession: A33705

A/Molecule type: DNA

A/Residues: 1-27 <BAS>

A/Cross-references: GB:J04821; NID:9182052; PIND:AA52379.1; PID:9553276
R/Fazio, M.J.; Olsen, D.R.; Kaub, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N

J. Invest. Dermatol. 91, 458-464, 1988

A/Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant

A/Reference number: A30524; MUID:89009960; PMID:3171221

A/Accession: A30524

A/Molecule type: mRNA

A/Residues: 1-453,483-617,651-792 <FA2>

A/Cross-references: EMBL:M36860; NID:9182061; PIND:AA52382.1; PID:9182062
R/Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenblum, J.;

Lab. Invest. 58, 270-277, 1988

A/Title: Isolation and characterization of human elastin cDNAs, and age-associated var

A/Reference number: A53891; MUID:88156138; PMID:2831431

A/Accession: A53891

A/Molecule type: mRNA

A/Residues: 164-453,483-500,507-617,651-792 <FA2>

A/Cross-references: GB:M24782; NID:9182063; PIND:AA53190.1; PID:9182064

C/Comment: The term tropoelastin refers to a soluble precursor form of the extracellular

line oxidase activity.

C/Genetics:

A/Gene: GDB:ELN

A/Cross-references: GDB:119107; OMIM:130160

A/Map position: 7q11.23-7q11.23

C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine

F.1-26/Domain: signal sequence #status predicted <SIG>

F.27-797/Product: elastin #status predicted <MAT>

F.782-787/Disulfide bonds: #status predicted

Query Match 100.0%; Score 501; DB 1; Length 792;
Best Local Similarity 100.0%; Pred. No. 4,2e-33;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAKSAKVAKAKQLRRAAGIGAGIPGLGVGVPGIGVGAGVGLGVGAGVPPFGAG 60
|||||
DB 559 VAAAKSAKVAKAKQLRRAAGIGAGIPGLGVGVPGIGVGAGVGLGVGAGVPPFGAG 618
|||||

QY 61 ADEGVRRLSPELREDDPSSQHLPTSPSSPRYPGALAAK 101
|||||
DB 619 ADEGVRRLSPELREDDPSSQHLPTSPSSPRYPGALAAK 659
|||||

RESULT 2
EAMS
elastin precursor - mouse
N/Alternate names: tropoelastin
C/Species: Mus musculus (house mouse)
C/Date: 18-Aug-1995 #sequence_rev1stion 16-Aug-1996 #text_change 09-Jul-2004
C/Accession: A55721
R/Wynder, K.S.; Sechler, J.L.; Boyd, C.D.; Passmore, H.C.
Genomics 23, 125-131, 1994
A/Title: Use of an intron length polymorphism to localize the tropoelastin gene to mouse
A/Reference number: A55721; MUID:95130069; PMID:7829060
A/Accession: A55721
A/Molecule type: mRNA
A/Residues: 1-860 <MYD>
A/Cross-references: UNIPROT:P54320; GB:U08210; NID:g473273; PIDN:AAA80155.1; PID:g473274
C/Genetics:
A/Map position: 5
C/Suprafamily: elastin
C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F/1-27/Domain: signal sequence #status predicted <SIG>
F/28-860/Product: elastin #status predicted <MNT>
F/850-855/Disulfide bonds: #status predicted

Query Match 52.9%; Score 265; DB 1; Length 860;
Best Local Similarity 60.6%; Pred. No. 4.4e-14;
Matches 60; Conservative 3; Mismatches 14; Indels 22; Gaps 3;

QY 3 AAASAKVAKAKQLRRAAGIGAGIPGLGVGVPGIGVGAGVPGFGAGAD 62
|||||
DB 592 AAASAKVAKAKQLRRAAGIGAGIPGLGVGVPGFGAGAD 650
|||||

QY 63 EGVRRRLSPELREDDPSSQHLPTSPSSPRYPGALAAK 101
|||||
DB 651 -GV-----PFGAG-----AVPGSLAAK 668
|||||

RESULT 3
EABO
elastin precursor, splice form a - bovine
N/Alternate names: tropoelastin
N/Contains: elastin precursor, splice form b; elastin precursor, splice form c
C/Species: Bos primigenius taurus (cattle)
C/Date: 08-Jun-1989 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: A31865; A26728; B6728; A22343; I45886
R/Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenblum, J.C.; Abrams,
Biochemistry 28, 2365-2370, 1989
A/Title: Structure of the bovine elastin gene and SI nuclease analysis of alternative sp
A/Reference number: A31865; MUID:89274159; PMID:2543440
A/Accession: A31865
A/Molecule type: DNA
A/Residues: 1-27 <YEH>
A/Cross-references: UNIPROT:P04985; UNIPROT:Q28101; GB:U02855; NID:g340504; PIDN:AAA3077
R/Raju, K.; Anwar, R.A.
J. Biol. Chem. 262, 5755-5762, 1987
A/Title: Primary structures of bovine elastin a, b, and c deduced from the sequences of
A/Reference number: A92640; MUID:87194772; PMID:3032943
A/Accession: A26728
A/Molecule type: mRNA
A/Residues: 1, 'RS', '4-11', 'E', '13-636', 'V', '638-747' <RAJ>
A/Cross-references: GB:U02717; NID:g163019; PIDN:AAA30503.1; PID:g163020

A/Accession: B26728
A/Molecule type: mRNA
A/Residues: 1, 'RS', '4-11', 'E', '13-225', '240-636', 'V', '638-747' <RA2>
A/Cross-references: GB:K03505; NID:g163025; PIDN:AAA30505.1; PID:g163026
A/Accession: C26728
A/Molecule type: mRNA
A/Residues: 1, 'RS', '4-11', 'E', '13-225', '260-636', 'V', '638-747' <RA3>
A/Cross-references: GB:K03506; NID:g163027; PIDN:AAA30506.1; PID:g163028
R/Cicilia, G.; May, M.; Ornstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rosenbl
Biochemistry 24, 3075-3080, 1985
A/Title: Structure of the 3' portion of the bovine elastin gene.
A/Reference number: A22343; MUID:85280426; PMID:2992576
A/Accession: A22343
A/Molecule type: DNA
A/Residues: 613-747 <CIC>
A/Cross-references: GB:M20415
R/Rosenblum, J.
Lab. Invest. 51, 605-623, 1984
A/Title: Biology of disease: Elastin: Relation of protein and gene structure to disease
A/Reference number: I45885; MUID:85059254; PMID:6150137
A/Accession: I45886
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 678-683, 685-747 <ROS>
A/Cross-references: GB:M31898; NID:g163015; PIDN:AAA36417.1; PID:g163018
R/Brown, P.L.; Mecham, L.; Tisdale, C.; Mecham, R.P.
Biochem. Biophys. Res. Commun. 186, 549-555, 1992
A/Title: The cysteine residues in the carboxy terminal domain of tropoelastin form an in
A/Reference number: A58621; MUID:92337651; PMID:1632791
A/Content: annotation, disulfide bonds
C/Comment: The term tropoelastin refers to a soluble precursor form of the extracellular
line oxidase activity.
C/Genetics:
A/Introns: 634/3; 653/3; 676/3; 689/3; 707/3; 716/3; 733/3
A/Note: the list of introns is incomplete
C/Suprafamily: elastin
C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F/1-747/Product: elastin precursor, splice form a #status predicted <EPA>
F/1-225,260-747/Product: elastin precursor, splice form c #status predicted <EPC>
F/1-225,260-747/Product: elastin precursor, splice form b #status predicted <EPB>
F/1-226/Domain: signal sequence #status predicted <SIG>
F/27-747/Product: elastin #status predicted <MNT>
F/105,109,252,271,275,324,327,400,404,407,445,448,489,493,544,548,552,606,609,645,649,66
F/737-742/Disulfide bonds: #status experimental

Query Match 52.8%; Score 264.5; DB 1; Length 747;
Best Local Similarity 59.4%; Pred. No. 4.2e-14;
Matches 60; Conservative 1; Mismatches 7; Indels 33; Gaps 1;

QY 1 VAAAKSAKVAKAKQLRRAAGIGAGIPGLGVGVPGIGVGAGVGLGVGAGVPPFGAG 60
|||||
DB 539 VPAASAKVAKAKQFRRAAGIPAGVPLGVGAGVPGIGVGAGVGLGVGAGVPPFGAG- 597
|||||

QY 61 ADEGVRRLSPELREDDPSSQHLPTSPSSPRYPGALAAK 101
|||||
DB 598 -----VPGTLAAK 606
|||||

RESULT 4
EART
elastin precursor - rat
N/Alternate names: tropoelastin
N/Species: Rattus norvegicus (Norway rat)
C/Date: 11-Jan-1991 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C/Accession: A36106; A30878; A36523; S02173; I54173; I66505
R/Pierre, R.A.; Deak, S.B.; Stolle, C.A.; Boyd, C.D.
Biochemistry 29, 9677-9683, 1990
A/Title: Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.
A/Reference number: A36106; MUID:91104868; PMID:1702999
A/Accession: A36106
A/Molecule type: mRNA
A/Residues: 1-864 <PIE>
A/Cross-references: UNIPROT:Q09372; GB:M60647; GB:U05292; NID:g207444; PIDN:AAA42269.1;

[illegible]

A:Accession: [P123456](#), [P123457](#), [P123458](#)
A:Molecule type: DNA
A:Residues: 1-1329 <RED>
A:Cross-references: UNIPROT:O86525, EMBL:AL031124, NID:e1332893, PID:e1332918, PIDN:CAAB

C/Superfamily:	glycine-rich RNA-binding protein; ribonucleoprotein repeat	homology
Query Match	20.7%;	Score 103.5; DB 2; Length 108;
Best Local Similarity	49.0%;	Pred. No. 0.067;

GenCore Version 5.1.6
Copyright (c) 1993-2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2005, 07:17:42 ; Search time 113.06 Seconds
(without alignments)
457.457 Million cell updates/sec

Title: US-09-743-818a-4_COPY_500_600

Perfect score: 501
Sequence: 1 VAAAKSAKVAKAQIRAA.....QHLPSTPSPRVGALAAAK 101

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	100.0	757	2	Q14234
2	501	100.0	757	2	Q75W05
3	493	98.4	635	2	O15336
4	304.5	60.8	658	2	Q9UMF5
5	304.5	60.8	643	2	O8NB14
6	304.5	60.8	687	2	O14235
7	304.5	60.8	687	2	Q72316
8	304.5	60.8	711	2	Q723F5
9	304.5	60.8	730	1	E1S_HUMAN
10	303.5	60.6	570	2	O6ZM6
11	300.5	60.0	472	2	O8N2G0
12	296.5	59.2	602	2	O15337
13	274.5	54.8	650	2	Q28039
14	274.5	54.8	666	2	Q28096
15	274.5	54.8	707	2	Q28098
16	269	53.7	679	2	O28097
17	265	52.9	810	2	Q9E829
18	265	52.9	860	1	E1S_MOUSE
19	265	52.9	860	1	Q8C9L8
20	264.5	52.8	747	1	E1S_BOVIN
21	249.5	49.8	864	1	E1S_RAT
22	219.5	43.8	658	1	O6P0L4
23	152.5	30.4	750	1	E1S_CHICK
24	142.5	28.4	1092	2	Q964R2
25	142	28.3	553	2	Q6ZUN2
26	132	26.3	279	2	Q6C3L2
27	130	25.9	907	2	Q26675
28	122	24.4	194	2	O6PY85
29	121.5	24.3	723	2	O9N107
30	117.5	23.5	897	2	O6O294
31	117	23.4	137	2	Q9GQX7

ALIGNMENTS

32	117	23.4	196	2	Q8PZF2	Q8PZF2 methanosarc
33	117	23.4	205	2	Q25946	Q25946 plasmodium
34	117	23.4	239	2	O6Z2M1	O6Z2M1 oryza sativ
35	117	23.4	1594	2	Q9VCW7	Q9VCW7 drosophila
36	117	23.4	1596	1	MAM_DROME	P21519 drosophila
37	114	22.8	5263	1	FBOH_BOMMO	P05790 bombyx mori
38	113	22.6	76	2	Q28100	Q28100 bos taurus
39	112.5	22.5	127	2	Q9PEK3	Q9PEK3 xylella fas
40	112.5	22.5	251	2	Q984T2	Q984T2 rhizobium l
41	112.5	22.5	912	2	Q9B1T2	Q9B1T2 plectreureys
42	112	22.4	301	2	Q01927	Q01927 phycophthor
43	111.5	22.3	103	2	Q7Z5D6	Q7Z5D6 homo sapien
44	111	22.2	156	2	Q9GQX6	Q9GQX6 plasmodium
45	111	22.2	343	2	Q01914	Q01914 phycophthor

RESULT 1

Q14234	PRELIMINARY;	PRT;	757 AA.
ID	Q14234		
AC	Q14234		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Elastin.		
GN	Name=ELN;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEBLINB=87274906; PubMed=3038460;		
RA	Indik Z., Yoon K., Morrow S.D., Cicilia G., Rosenbloom J.,		
RA	Rosenbloom U., Ornstein-Goldstein N., Sheppard P., Anderson N.,		
RT	"Structure of the 3' region of the human elastin gene: great abundance		
RT	of Alu repetitive sequences and few coding sequences.";		
RL	Connect. Tissue Res. 16:197-211(1987).		
DR	EMBL; M17282; AAC98395.1; -		
DR	EMBL; M16983; AAC98395.1; JOINED.		
DR	EMBL; M17265; AAC98395.1; JOINED.		
DR	EMBL; M17265; AAC98395.1; JOINED.		
DR	EMBL; M17267; AAC98395.1; JOINED.		
DR	EMBL; M17268; AAC98395.1; JOINED.		
DR	EMBL; M17270; AAC98395.1; JOINED.		
DR	EMBL; M17271; AAC98395.1; JOINED.		
DR	EMBL; M17272; AAC98395.1; JOINED.		
DR	EMBL; M17273; AAC98395.1; JOINED.		
DR	EMBL; M17274; AAC98395.1; JOINED.		
DR	EMBL; M17275; AAC98395.1; JOINED.		
DR	EMBL; M17276; AAC98395.1; JOINED.		
DR	EMBL; M17277; AAC98395.1; JOINED.		
DR	EMBL; M17278; AAC98395.1; JOINED.		
DR	EMBL; M17279; AAC98395.1; JOINED.		
DR	EMBL; M17280; AAC98395.1; JOINED.		
DR	EMBL; M17281; AAC98395.1; JOINED.		
DR	GO; GO:0005578; C:extracellular matrix (sensu Metazoa); NAS.		
DR	GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.		
DR	InterPro; IPR001451; Hexapep_transf.		
DR	InterPro; IPR003979; tropoelastin.		
DR	PRINTS; PR01500; TROP0ELASTIN.		
DR	PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.		
SO	SEQUENCE	757 AA;	66136 MW; 2387FE5B8A8F5C8_CRC64;

Query Match 100.0%; Score 501; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 8.6e-28;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAAAKSAKVAKAAQLRRAAGIGAGIPGLGVGVPGIGVGAGVPGIGVAGVPGFGAG 60
DB 524 VAAAAAKSAKVAKAAQLRRAAGIGAGIPGLGVGVPGIGVGAGVPGIGVAGVPGFGAG 583

QY 61 ADEGVRRLSPELRECDPSSQHLPTSPSPRPVPGALAAK 101
DB 584 ADEGVRRLSPELRECDPSSQHLPTSPSPRPVPGALAAK 624

RESULT 2
ID Q9UMF5 PRELIMINARY; PRT; 757 AA.
AC Q95M05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein ELN.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
Wylye G.A., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
Vandrunft A., Nguyen C., Du F., Lamar B., Courtney J., Kalicki J.,
Razzerky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
Kozlowski-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
Tin-Mollam A.M., Abbott A., Mink P., Maupin R., Strommatt C.,
Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
Wendt M.C., Yang S.P., Schultz B.R., Wallis J.W., Spielh J.,
Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,
Hickobotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E.,
Gillett W., Zhou Y., James R., Phelps K., Iadonato S., Bub K.,
Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
Baerisch R.A., Brent M.R., Keibler E., Filcek P., Bork P., Suyama M.,
Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Ghosh W.R.,
Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RN Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Wilson R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005056; AAS07435.1; -;
DR GO; GO:0005578; Extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005201; Extracellular matrix structural constituent, IEA.
DR InterPro; IPR001451; Hexapep_transf.
DR PRINTS; PRO1500; TROPOLASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;

Query Match 100.0%; Score 501; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 8.6e-28;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAAAAAKSAKVAKAAQLRRAAGIGAGIPGLGVGVPGIGVGAGVPGIGVAGVPGFGAG 60
DB 524 VAAAAAKSAKVAKAAQLRRAAGIGAGIPGLGVGVPGIGVGAGVPGIGVAGVPGFGAG 583

QY 61 ADEGVRRLSPELRECDPSSQHLPTSPSPRPVPGALAAK 101
DB 584 ADEGVRRLSPELRECDPSSQHLPTSPSPRPVPGALAAK 624

RESULT 3
ID O15336 PRELIMINARY; PRT; 635 AA.
AC O15336;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Elastin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97358574; PubMed=9215670; DOI=10.1093/hmg/6.7.1021;
RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
Morris C.A., Keating M.T.;
RT "Elastin point mutations cause an obstructive vascular disease,
supravalvular aortic stenosis.";
RL Hum. Mol. Genet. 6:1021-1028(1997).
DR EMBL; U93037; AAB65621.1; JOINED.
DR EMBL; U93034; AAB65621.1; JOINED.
DR EMBL; U93035; AAB65621.1; JOINED.
DR EMBL; U93036; AAB65621.1; JOINED.
GO; GO:0005578; Extracellular matrix (sensu Metazoa); IEA.
GO; GO:0005201; Extracellular matrix structural constituent, IEA.
DR InterPro; IPR001451; Hexapep_transf.
DR PRINTS; PRO1500; TROPOLASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
FT NON TER 1
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 635 AA; 55279 MW; 72950C36412782A4 CRC64;

Query Match 98.4%; Score 493; DB 2; Length 635;
Best Local Similarity 99.0%; Pred. No. 2.7e-27;
Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VAAAAAKSAKVAKAAQLRRAAGIGAGIPGLGVGVPGIGVGAGVPGIGVAGVPGFGAG 60
DB 531 VAAAAAKSAKVAKAAQLRRAAGIGAGIPGLGVGVPGIGVGAGVPGIGVAGVPGFGAG 590

QY 61 ADEGVRRLSPELRECDPSSQHLPTSPSPRPVPGALAAK 101
DB 591 ADEGVRRLSPELRECDPSSQHLPTSPSPRPVPGALAAK 631

RESULT 4
ID Q9UMF5 PRELIMINARY; PRT; 258 AA.
AC Q9UMF5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Elastin (Fragment).
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

	RX	MEDLINE=96411691; PubMed=8812460; DOI=10.1006/geno.1996.0469;
	RA	Osborne L.R., Mattidale D.W., Scherer S.W., Shi X.-M., Huizenga J.,
	RA	Heng H.H.Q., Costa T., Rober B., Lew L., Brinkman J., Rommens J.,
	RT	"Koep B.F., Tsui L.C.;
	RT	"Identification of genes from a 500-kb region at 7q11.23 that is
	RT	commonly deleted in Williams syndrome patients.";
	RL	Genomics 36:328-336(1996).
	RN	[2]
	RP	SEQUENCE FROM N.A.
	RX	MEDLINE=20458668; PubMed=11003705;
	RA	Mattidale D.W., Wilson M.D., Wang D., Burke R.D., Chen X.,
	RA	Duronto V., Koop B.F.;
	RT	"Comparative genomic sequence analysis of the Williams syndrome region
	RT	(LIMK1-RFC2) of human chromosome 7q11.23."
	RL	Mamm. Genome 11:890-898(2000).
	DR	EMBL; U63721; AACI384.1; -.
	DR	InterPro; IPR001451; Hexapet_transf.
	DR	PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
	FT	NON TER
	SQ	SEQUENCE 258 AA; 21990 MW; C39BF7298D0B05D2 CRC64;
	Query Match	60.8%; Score 304.5; DB 2; Length 258;
	Best Local Similarity	67.3%; Pred. No. 2.9e-14;
	Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;	
Oy	1	VAAAKSAKVAAKQLRAAAGLGAGTGTGCTGGVGVPGTGGAGVPGLGVAGVPGFAG 60
Db	58	VAAAASAKVAAKQLRAAAGLGAGTGTGCTGGVGVPGTGGAGVPGLGVAGVPGFAG- 116
Oy	61	ADEGVRSLSPELRREGDPSSSOHLPTSTSPSPVPALAAK 101
Db	117	-----VPGALAAK 125
	RESULT 5	
	OSNB14	
	ID OSNB14	PRELIMINARY; PRT; 643 AA.
	AC OSNB14;	
	DT 01-OCT-2002 (TREMBLrel. 22, Created)	
	DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)	
	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
	DE Hypothetical protein PSEC0254.	
	OC Homo sapiens (Human).	
	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
	OX NCBI_TaxID=9606;	
	RN [1]	
	RP SEQUENCE FROM N.A.	
	RA Ota T., Mishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,	
	RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,	
	RA Nagahara K., Sugano S., Isogai T.;	
	RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
	DR EMBL; AK075554; BA011696.1; -.	
	DR HSRP; P50099; 1ZRF.	
	DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.	
	DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.	
	DR InterPro; IPR001451; Hexapep_transf.	
	DR InterPro; IPR003979; tropoelectin.	
	DR PRINTS; PR01500; TROPOELASTIN.	
	DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.	
	SQ SEQUENCE 643 AA; 55629 MW; FDP0C42617E72A69 CRC64;	
	Query Match	60.8%; Score 304.5; DB 2; Length 643;
	Best Local Similarity	67.3%; Pred. No. 6.3e-14;
	Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;	
Oy	1	VAAAKSAKVAAKQLRAAAGLGAGTGTGCTGGVGVPGTGGAGVPGLGVAGVPGFAG 60
Db	443	VAAAASAKVAAKQLRAAAGLGAGTGTGCTGGVGVPGTGGAGVPGLGVAGVPGFAG- 501
Oy	61	ADEGVRSLSPELRREGDPSSSOHLPTSTSPSPVPALAAK 101
Db	502	-----VPGALAAK 510

```

RESULT 6
ID      014235          PRELIMINARY;       PRT;       687 AA.
AC      014235;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Blastin.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=87289668; PubMed=3038460;
RA      Indik Z., Yoon K., Morrow S.D., Cicilia G., Rosenblum J.,
RA      Rosenblum U., Ornstein-Goldstein N.;
RT      "Structure of the 3' region of the human elastin gene: great abundance
RT      of Alu repetitive sequences and few coding sequences.";
RL      Connect. Tissue Res. 16:197-211(1987).
DR      EMBL; M17282; AAC98393.1; JOINED.
DR      EMBL; M16983; AAC98393.1; JOINED.
DR      EMBL; M17265; AAC98393.1; JOINED.
DR      EMBL; M17266; AAC98393.1; JOINED.
DR      EMBL; M17267; AAC98393.1; JOINED.
DR      EMBL; M17268; AAC98393.1; JOINED.
DR      EMBL; M17271; AAC98393.1; JOINED.
DR      EMBL; M17272; AAC98393.1; JOINED.
DR      EMBL; M17273; AAC98393.1; JOINED.
DR      EMBL; M17275; AAC98393.1; JOINED.
DR      EMBL; M17276; AAC98393.1; JOINED.
DR      EMBL; M17277; AAC98393.1; JOINED.
DR      EMBL; M17278; AAC98393.1; JOINED.
DR      EMBL; M17279; AAC98393.1; JOINED.
DR      EMBL; M17281; AAC98393.1; JOINED.
DR      HSBP; P50099; IZFU.
DR      GO; GO:0005578; Cytoskeletal matrix (sensu Metazoa); NAS.
DR      GO; GO:0030023; Extracellular matrix constituent conferring. . .; NAS.
DR      InterPro; IPR001455; Hexapep_transf.
DR      InterPro; IPR003979; Tropoelastin.
DR      PRINTS; PR01500; TROPOELASTIN.
DR      PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SQ      SEQUENCE 687 AA; 59525 MW; 864068C4C8E9F88F CRC64;

Query Match      60.8%; Score 304.5; DB 2; Length 687;
Best Local Similarity 67.3%; Pred. No. 6,6e-14;
Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1

QY      1 VAAAAAQAQAAQAQALRAAGIGAGIPGLGVGCVPGIAGVAGVPGIGAGVPGFGAG 60
DB      505 VAAAASAAAVAAKKAOLRAAGIGAGIPGLGVGCVPGIAGVAGVPGIGAGVPGFGA- 565
QY      61 ADEGVRSLSPELRBDPSSSCHLPDTPSPRVPALAAAK 101
DB      564 -----VPGALAAAK 572

RESULT 7
ID      072316          PRELIMINARY;       PRT;       687 AA.
AC      072316;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
```

DT 01-OCT-2003 (Tremblrel. 25, last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
 DE Hypothetical protein DKFZp66021208 (Fragment).
 GN Name=DKFZp66021208;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RA Lauber J., Bahr A., Mewes H.W., Weill B., Amid C., Oeanger A., Fobo G.,
 Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX53199; CAD98065.1; -;
 DR InterPro; IPR001451; Hexapep.transf.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERSSES; UNKNOWN_1.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 687 AA; 59847 MW; 79232A19DC1F10F CRC64;

Query Match 60.8%; Score 304.5; DB 2; Length 687;
 Best Local Similarity 67.3%; Pred. No. 6.6e-14;
 Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

OY 1 VAAASAKVAAKQAOLRAAGAGIPGLGVGVGPGAGVGLGVGAGVPGFAG 60
 DB 505 VAAASAKVAAKQAOLRAAGAGIPGLGVGVGPGAGVGLGVGAGVPGFAG- 563
 OY 61 ADEGVRSLSPELREGDPSSQHLPTSPSPRVPGLAALK 101
 DB 564 -----VPGALAAK 572

RESULT 8
 ID Q723F5 PRELIMINARY; PRT; 711 AA.
 AC Q723F5;
 DT 01-OCT-2003 (Tremblrel. 25, last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, last sequence update)
 DE Hypothetical protein DKFZp66021208.
 GN Name=DKFZp66021208;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human fetal kidney;
 RA Pouskka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 Mewes H.W., Weill B., Amid C., Oeanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX537939; CAD97910.1; -;
 DR InterPro; IPR001451; Hexapep.transf.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERSSES; UNKNOWN_1.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 711 AA; 61765 MW; 95B624A93BA9998 CRC64;

Query Match 60.8%; Score 304.5; DB 2; Length 711;
 Best Local Similarity 67.3%; Pred. No. 6.8e-14;
 Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;
 OY 1 VAAASAKVAAKQAOLRAAGAGIPGLGVGVGPGAGVGLGVGAGVPGFAG 60
 DB 529 VAAASAKVAAKQAOLRAAGAGIPGLGVGVGPGAGVGLGVGAGVPGFAG- 587
 OY 61 ADEGVRSLSPELREGDPSSQHLPTSPSPRVPGLAALK 101
 DB 588 -----VPGALAAK 596

RESULT 9

ELS_HUMAN
 ID ELS_HUMAN STANDARD; PRT; 730 AA.
 AC P15502; Q14233; Q14238;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Elastin precursor (tropoelastin).
 GN Name=ELS;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RX MEDLINE=87289668; PubMed=3039501;
 RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
 Rosenbloom J.C., Peltonen L., Rosenbloom J.;
 RT "Alternative splicing of human elastin mRNA indicated by sequence analysis of cloned genomic and complementary DNA."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=skin fibroblast;
 RX MEDLINE=89009960; PubMed=3171221;
 RA Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z.,
 Ornstein-Goldstein N., Yeh H., Rosenbloom J., Utito J.;
 RT "Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant cDNA library: further elucidation of alternative splicing utilizing exon-specific oligonucleotides."
 RL J. Invest. Dermatol. 91:458-464(1988).
 RN [3]
 RP SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).
 RC TISSUE=Placenta;
 RX MEDLINE=88156138; PubMed=2831431;
 RA Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
 Rosenbloom J., Utito J.;
 RT "Isolation and characterization of human elastin cDNAs, and age-associated variation in elastin gene expression in cultured skin fibroblasts."
 RL Lab. Invest. 58:270-277(1988).
 RN [4]
 RP SEQUENCE OF 603-730 FROM N.A.
 RC TISSUE=Hipocampus; and Placenta;
 RX MEDLINE=96291399; PubMed=8689688; DOI=10.1016/S0092-8674(00)80077-X;
 RA Frangiskakis J.M., Ewart A.K., Morris C.A., Meyers C.B., Bertrand J., Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green E.D., Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J., Keating M.T.;
 RT "LIM-kinase hemizyosity implicated in impaired visuospatial constructive cognition."
 RL Cell 86:59-69(1996).
 RN [5]
 RP INVOLVEMENT IN CUTIS LAXA.
 RX MEDLINE=99091639; PubMed=9873040; DOI=10.1074/jbc.274.2.981;
 RA Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;
 RT "Cutis laxa arising from frameshift mutations in exon 30 of the elastin gene (ELN)."
 RL J. Biol. Chem. 274:981-986(1999).
 RN [6]
 RP INVOLVEMENT IN SVAS.
 RX PubMed=10942104;
 RA Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P., Munich A., Bykens B., Gewillig M., Devriendt K., Boyd C.D.;
 RT "Isolated supravalvular aortic stenosis: functional haploinsufficiency of the elastin gene as a result of nonsense-mediated decay."
 RL Hum. Genet. 106:577-588(2000).
 CC -1- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.
 CC -1- SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.
 CC -1- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=P15502-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P15502-2; Sequence=VSP_004243;
 CC -1- P15502-2; Sequence=VSP_004243;
 CC -1- DISEASE: Defects in ELN are a cause of autosomal dominant cutis
 CC laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder
 CC characterized by loose, hyperextensible skin with decreased
 CC resilience and elasticity leading to a premature aged appearance.
 CC The skin changes are often accompanied by extracutaneous
 CC manifestations, including pulmonary emphysema, bladder
 CC diverticula, pulmonary artery stenosis and pyloric stenosis.
 CC -1- DISEASE: Haploinsufficiency of ELN may be the cause of certain
 CC cardiovascular and musculo-skeletal abnormalities observed in
 CC Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare
 CC developmental disorder and a contiguous gene deletion syndrome
 CC involving genes from chromosome band 7q11.23.
 CC -1- DISEASE: Defects in ELN are the cause of supravalvular aortic
 CC stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of
 CC the ascending aorta which can occur sporadically, as an autosomal
 CC dominant condition, or as one component of Williams-Beuren
 CC syndrome.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, M17282; AAC98394.1; -;
 CC EMBL, M16983; AAC98394.1; JOINED.
 CC EMBL, M17265; AAC98394.1; JOINED.
 CC EMBL, M17266; AAC98394.1; JOINED.
 CC EMBL, M17267; AAC98394.1; JOINED.
 CC EMBL, M17268; AAC98394.1; JOINED.
 CC EMBL, M17270; AAC98394.1; JOINED.
 CC EMBL, M17271; AAC98394.1; JOINED.
 CC EMBL, M17272; AAC98394.1; JOINED.
 CC EMBL, M17273; AAC98394.1; JOINED.
 CC EMBL, M17274; AAC98394.1; JOINED.
 CC EMBL, M17275; AAC98394.1; JOINED.
 CC EMBL, M17276; AAC98394.1; JOINED.
 CC EMBL, M17277; AAC98394.1; JOINED.
 CC EMBL, M17278; AAC98394.1; JOINED.
 CC EMBL, M17279; AAC98394.1; JOINED.
 CC EMBL, M17280; AAC98394.1; JOINED.
 CC EMBL, M17281; AAC98394.1; JOINED.
 CC EMBL, M36860; AAAS2382.1; -;
 CC EMBL, M24782; AAAS1190.1; -;
 CC EMBL, U62292; AAB17544.1; -;
 CC EMBL, X15603; CAA33627.1; -;
 CC PIR: A33707; EAHU
 CC HSSP: P50099; 1ZFU
 CC GeneW: HGNC:3327; ELN.
 CC MIM: 130160; -;
 CC MIM: 123700; -;
 CC MIM: 194050; -;
 CC MIM: 185500; -;
 CC GO: GO:0005578; C:extracellular matrix; TAS.
 CC GO: GO:0005615; C:extracellular space; TAS.
 CC GO: GO:0005201; F:extracellular matrix structural constituent; TAS.
 CC GO: GO:0008283; P:cell proliferation; TAS.
 CC GO: GO:0008015; P:circulation; TAS.
 CC GO: GO:0009887; P:organogenesis; TAS.
 CC GO: GO:0007585; P:respiratory gaseous exchange; TAS.
 CC InterPro: IPR003979; tropoelastin.
 CC PRINTS: PR01500; TROPOLASTIN.
 CC Alternative splicing; Repeat; Signal; Structural protein;
 CC Williams-Beuren syndrome.
 CC SIGNAL 1 26
 CC FT CHAIN 27 730 Elastin.

FT DISUPID 720 725 By similarity.
 FT VARSPIC 472 477 Missing (in isoform 2).
 FT /Ftd=VSP_004243.
 SQ SEQUENCE 730 AA; 63260 MW; AB06D15BA567AA46 CRC64;
 : Query Match 60.8%; Score 304.5; DB 1; Length 730;
 : Best Local Similarity 67.3%; Pred. No. 7e-14;
 : Matches 68; Conservative 0; Mismatches 0; Indels 33; Gaps 1;
 QY 1 VAAASAAKVAKADLRRAAGGAGTIGLVGVGVPGIGVGVGPGIGVGVGPGAG 60
 DB 530 VAAASAAKVAKADLRRAAGGAGTIGLVGVGVPGIGVGVGPGIGVGVGPGAG 588
 QY 61 ADEGVRRSLPELRGDPSSQHLPTSPSPRYGALAANK 101
 DB 589 -----VFGALAAAK 597
 RESULT 10
 06ZMJ6 PRELIMINARY; PRT; 570 AA.
 AC 06ZMJ6;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein FLJ16246.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
 RA Wakebe H., Ono T., Hishigaki H., Matanabe T., Ozaki K., Sugiyama T.,
 RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
 RA Isono Y., Kawai-Hito Y., Saito K., Nishikawa T., Kimura K.,
 RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Magatsuna M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
 RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahata K.,
 RA Masuno Y., Nagai K., Isogai T.,
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK122731; BAC85506.1; -;
 DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO: GO:0005201; F:extracellular matrix structural constituent; IEA.
 DR InterPro: IPR001451; Hexapep_transf.
 DR PRINTS: PR01500; TROPOLASTIN.
 DR PROSITE: PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
 SQ SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B CRC64;
 Query Match 60.6%; Score 303.5; DB 2; Length 570;
 Best Local Similarity 66.3%; Pred. No. 6.7e-14;
 Matches 67; Conservative 1; Mismatches 0; Indels 33; Gaps 1;
 QY 1 VAAASAAKVAKADLRRAAGGAGTIGLVGVGVPGIGVGVGPGIGVGVGPGAG 60
 DB 388 VAAASAAKVAKADLRRAAGGAGTIGLVGVGVPGIGVGVGPGIGVGVGPGAG 446
 QY 61 ADEGVRRSLPELRGDPSSQHLPTSPSPRYGALAANK 101
 DB 447 -----VFGALAAAK 455
 RESULT 11
 08N2G0 PRELIMINARY; PRT; 472 AA.
 AC 08N2G0;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein PSEC0191.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia Eutheria; Primates; Catarrhini, Homiinae; Homo.
OX NCPI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=whole embryo;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK075494; BAC11651.1; -
DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO: GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep_tranf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROP0ELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASIS; UNKNOWN_1.
DR NON_TER 472
SQ SEQUENCE 472 AA; 42265 MW; 8D7A0F3A9BF971F3 CRC64;

Query Match	60.0%	Score 300.5	DB 2	Length 472
Best Local Similarity	66.3%	Pred. No. 9,3e-14		
Matches	67	Conservative 0	Mismatches 33	Gaps 1
QY	1	VAAAKSAKAAKAAKQLRRAAGLGGGIGTGGVGPGLGVAGVPGIGVAGVGPFGAG	60	
Db	298	VAAAKSAKAAKAAKQLRRAAGLGGGIGTGGVGPGLGVAGVPGIGVAGVGPFGAG	356	
QY	61	ADEGVRRSLPELRGDPSSQHLPSTSSPPVPGALAAK	101	
Db	357	-----VPGALAAK	365	

RESULT 12
015337
ID 015337 PRELIMINARY; PRT; 602 AA.

DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 25, Last annotation update)
DE Elastin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
CX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97355574; PubMed=9215670; DOI=10.1093/hmg/6.7.1021;
RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.
RT "Elastin point mutations cause an obstructive vascular disease,
RT supravalvular aortic stenosis.".
RL Hum. Mol. Genet. 6:1021-1028(1997).
DR EMBL; U93037; AAB65620.1; -.
DR EMBL; U93034; AAB65620.1; JOINED.
DR EMBL; U93035; AAB65620.1; JOINED.
DR EMBL; U93036; AAB65620.1; JOINED.
DR CO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep_tcnst.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; P00150; TROP0ELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERSSES; UNKNOWN_1.
FT NON_TER 1 1
SQ SEQUENCE 602 AA; 51807 MW; 53B5B9A71EF04B07 CRC64;

Query Match	Score	DB	Length
59.2%	296.5	2	602
Similarity	Pred.	No.2=13	
Best Local	66.3%		
Matches	67	Conservative	1
		Indels	33
		Gaps	1

Qy	1	VAAAKSAKVAQAQQLRAAAGLGGAGIPGLGAGVGVPGLGAGVPGGLGAGVPGFGAG	60
Db	531	VAAAKSAKVAQAQQLRAAAGLGGAGIPGLGAGVGVPGLGAGVPGGLGAGVPGFR-	589

QY	61	ADEGVRSLSP	ELREGDPSSQHL	PSTPSSPRV	PGALAAAK	101
Db	590	-----	-----	VP	GA	598
				LA	AA	
				AK		

RESULT 13		
Q28099		
ID	Q28099	PRELIMINARY; PRT; 650 AA.
AC	Q28099;	
DT	01-NOV-1996 (TREMBLrel. 01, Created)	
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
DE	Elastin-CBELL; NCBI gi: 163003 (Fragment).	
OS	Bos taurus (Bovine).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
OC	Bovinae; Bos.	
OX	NCBI_TaxID=9913;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=85280426; Pubmed=29932576;	
RA	Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,	
RA	Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;	
RT	"Structure of the 3' portion of the Bovine elastin gene.";	
RL	Biochemistry 24:3075-3080 (1985).	
RN	[2]	

RP SEQUENCE FROM N.A.
RX MEDLINE=88028442; PubMed=36655402;
RA Yeh H., Ornestein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
R Rosenbloom J.C., Cicilia G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
RT splicing."
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30499.1; JOINED.
DR EMBL; M11422; AAA30499.1; JOINED.
DR EMBL; M19366; AAA30499.1; JOINED.
DR EMBL; M19368; AAA30499.1; JOINED.
DR EMBL; M19369; AAA30499.1; JOINED.
DR EMBL; M19370; AAA30499.1; JOINED.
DR EMBL; M19371; AAA30499.1; JOINED.
DR EMBL; M22771; AAA30499.1; JOINED.
DR EMBL; M22772; AAA30499.1; JOINED.
DR EMBL; M22773; AAA30499.1; JOINED.
DR EMBL; M22774; AAA30499.1; JOINED.
DR EMBL; M22775; AAA30499.1; JOINED.
DR EMBL; M22988; AAA30499.1; JOINED.
DR GO; M23010; AAA30499.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPRO00197; tropoelastin.
DR PRINTS; PR01500; TROPELASTIN.
SQ SEQUENCE 650 AA; 55373 MW; CD21AB83E9076AD7 CRC64;
FT NON TER 1 1

Query Match	54.8%	Score 274.5	DB 2	Length 650
Best Local Similarity	60.4%	Pred. No. 8.5e-12		
Matches	61	Conservative 1	Mismatches 6	Indels 33
			Gaps 1	
QY	1 VAAAAKSAKAAKAAQQLPAAAGCAGCAGCGVGVGVPGLGVGAAGVPGIGVGAAGVPGAG	60		
DB	450 VPAAKSAKAAKAAKAAQCPRAAGCAGCAGCGVGVGVPGLGVGAGVPGIGVGAAGVPGCA	508		
QY	61 ADEGVRRSLPELREGDPSSQHLPSPTSSPRVPGALAAK	101		
DB	509 -----VEGTALAAK	517		

RESULT 14	
Q28096	PRELIMINARY; PRT; 666 AA.
ID Q28096	
AC Q28096;	
DT 01-NOV-1996 (TREMBLrel. 01, Created)	

THIS PAGE IS BLANK